STIC-Biotech/ChemLib

184368

From:

Portner, Ginny

Sent:

Wednesday, April 05, 2006 2:30 PM

To:

STIC-Biotech/ChemLib

Subject: 10/768,093

please search SEQ Id No 9 and 4 with respect to polypeptide/amino acid sequences.

Ginny Portner Remsen Building Art Unit 1645

Room E03, B02; Mail Box 3C18

(571) 272-0862

APR -5 2005

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Title:
Perfect score:
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O809165_CAEEL
O09165_CAEEL
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            NUCLEOTIDE SEQUENCE.
STRAIN=0167:H5 / E10703 / EIEC;
Wolf M.K., de Haan L., Cassels F.C.
Gaastra W., Warren R., Boedeker E.C.
Submitted (JAN-1994) to the EMBL/Ge
                                                                                                                                                      F6B1_ECOLI STANDARD; PRT; 167 AA. P53510; PCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update) CS6 fimbrial subunit B precursor.
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Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Fimbriae (also called pili), polar filaments radia from the surface of the bacterium to a length of 0.5-1.5 micrometers and numbering 100-300 per cell, enable bacteria colonize the epithelium of specific host organs.
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01-OCT-1996 (Rel. 34, Last sequence up
10-MXY-2005 (Rel. 47, Last annotation
CS6 fimbrial subunit A precursor (CS6
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Enterobacteriaceae; Escherichia.
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Enterobacteriaceae; Escherichia.
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Pred. No. 1.4e-52;
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CS6 fimbrial subunit A.
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Wolf M.K., de Haan L.A.M., Cassels F.C., Willshaw G.A.,
Gaastra W., Warren R., Boedeker E.C.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
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PIR; 183348; 183348.
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                  VYDEDYGLGRLVNTADASOSIIYQIVDEKGKKMLKDHGA------
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LTSSGQQIGKLVNVNNPDQNMNYYI-----RKDSGAGNFMAGQKGSFPVKENTSYTF
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KALNYTSGE---KKISPGIYNDQVMVGYYVN 136

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RESULT 6
Q72P30 LE
ID P30 P3P
AC Q72P
DT 05-J
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RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Bankier K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Kooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Mardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
Loulseged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Loulseged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Loulseged H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Milliams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
"The genome of the social amoeba Dictyostelium discoideum.";
Nature O. On 2005)
                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dictyostellum discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum
NCBI_TaxID=44689;
                                                    Membrane carboxypeptidase. OrderedLocusNames=LIC12646;
                                                                                   05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                    Q72P30_LEPIC PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.
EMBL; AAFI01000071; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 0:0-0(2005).
-I- CAUTION: The sequence shown here EMBL/GenBank/DDBJ whole genome sh
 Copenhageni).
Bacteria; Spirochaetes;
                                Leptospira interrogans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
ORFNames=DDB0215209;
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                                                                                                                                                                                                                                                 GVKIGYHHSGNVLENMESKKLPFKKENYDKVKGYVGE--YMPGLNNDKEGHSVVCHYTN
                                                                                                                                                                                                                                                                                                                                                   VNLTVPENVSQVTVYPVYDEDYGLGRLVNTADASQ-----SIIYQ-----IVDEK 88
                                                                                                                                                                                                                                                                                GKKMLKDHGAEVTPN---QQITFKALNYTS----
                                                                                                                                                                                                                                                                                                                    LNITLPLEISQETVF-----YWEPKLNNTIDYTQFNNPVSIFYDNNSDVYYSLPQIDVK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                            al protein.
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                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            50234 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         13.2%;
30.3%;
                                  (serogroup Icterohaemorrhagiae /
 Spirochaetales; Leptospiraceae;
                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                       Last sequence update)
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Last annotation update)
                                                                                                                         Created)
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Pred. No. 6.4;
6; Mismatches :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             shotgun (WGS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is derived from an
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     Leptospira
                                       Berovar
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A Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,
A Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,
RA Kuramae E.E., Lemos B.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
"Comparative genomics of two Leptospira interrogans serovars reveals
"Comparative genomics of two Leptospira interrogans serovars reveals
"Tovel insights into physiology and pathogenesis.";
J. Bacteriol. 186:2164-2172(2004)

DB GOES J. Bacteriol. 186:2164-2172(2004)

DR GOGO0003274; C:cell wall (sensu Bacteria); IEA.
DR GO; GO:0003274; P:caraboxypeptidase activity; IEA.
DR GO; GO:0003284; P:centalytic activity; IEA.
DR GO; GO:0003284; P:penicillin binding; IEA.
DR GO; GO:0003252; P:peptidoglycan biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 37
STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai; MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597; Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H., Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-U., Jia J., Tu Y.-F. Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F., Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma Y., Cai Z., Sheng Y., Zhu G.-F., Wan M., Huang H.-L., Gian Z., Wang S.-Y., Mang Y.-Q., Xia Q.-C., Guo X.-K., Danchin M., Saint Girons I., Somerville R.U., Wen Y.-M., Shi M.-H., Chen Z., Xu J.-G., Zhao G.-P.;
                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sanotation update)
Penicillin-binding protein 1A (EC 3.4.-.-) (EC 2.4.2.-)
OrderedLocusNames=LA1009;
                                                                                                                                                                                                                                                                                                                                                                                                                           D7_LEPIN
Q8F7D7_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001264; Glyco_trans_51.
InterPro; IPR001460; Penncl_bind_tpept.
Pfam; PP009012; Transgly; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Glyco_trans_51; 1.
ProDom; PD001895; Glyco_trans_51; 1.
Carboxypeptidase; Complete proteome.
SEQUENCE 918 AA; 102807 MW; 2D9E53;
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Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
No P.L., Haake D.A., Verjovski Almeida S., Hartskeerl R.A.,
Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
Coutinho L.L., Degrave W.M., Dellagostin O.A., El-Dorry H.,
Coutinho E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Giglioti E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                     Q8F7D7
                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                           Bacteria;
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                                                                                                                                                                                                                                  NCBI_TaxID=173;
                                                                                                                                                                                                                                                                             septospira interrogans.
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                                                                                                                                                                                                                                                                                                                                                                                                                      _LEPIN PRELIMINARY;
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37; Conserv
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                                                                                                                                                                                                                                                           Spirochaetes;
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                                                                                                                                                                                                                                                           Spirochaetales; Leptospiraceae; Leptospira.
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Pred. No.
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                                                                                                                  Y.-F.,
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Best Local
                                                  InterPro; IPR005949; Form_actrans GR
InterPro; IPR001150; Form_actrans GR
InterPro; IPR004184; Pyr_Form_lyase.
Pfam; PF01228; Gly_radical; 1.
Pfam; PF02901; PFL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIJINE-25608415; PubMed=12721630; DOI=10.1038/nature01582; MEDIJINE-25608415; PubMed=12721630; DOI=10.1038/nature01582; Tvanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Golteman E., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence)
01-CCT-2003 (TrEMBLrel. 25, Last annotat.
Formate acetyltransferase (EC 2.3.1.54).
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QB1IA3_BACCR PRELIMINARY;
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NCBI_TaxID=226900;
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InterPro; IPR001460; Pencl_bind_tpept.
Pfam; PF00912; Transgly; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Glyco_trans_51; 1.
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Overbeek R., Kyrpides N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus cereus (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=BC0491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome sequence of Bacillus cereus and comparative analysis with
                                                                                                                                                                               GO:0005737; C:cytoplasm; IEA.
GO:0008415; F:acyltransferase activity; IEA.
GO:0008661; F:cormate C-acetyltransferase activity;
GO:0016740; F:transferase activity; IEA.
GO:0005975; P:carbohydrate metabolism; IEA.
GO:000606; P:glucose metabolism; IEA.
GO:0008152; P:metabolism; IEA.
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L; AE011285; AAN48208.1; -; Genomic DNA.
GO:0009274; C:cell wall (sensu Bacteria);
GO:0003824; F:catalytic activity; IEA.
GO:0008658; F:penicillin binding; IEA.
GO:0008658; P:peptidoglycan biosynthesis;
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                                                                                                                                                                                                                                                                                                                                                                                         AE016999; AAP07529.1; -; Genomic_DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                   423:87-91 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GLGRLVNT-----ADASQSIIYQIVDEKGKKMLKDHGAEVTPNQQITFKA---LNYT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGFSIYTTVSEPVQAELPKIVKNYVDNVQKNG-LVRKTRLTDNKNSSETAVFRRYIQDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         revealed by
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55; pyr form_ly_1; 1.
GLY_RADICAL; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 87; DB:
Pred. No. 44;
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEEA6FD48DC58326 CRC64;
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Query Match
                                                                                                                                                                                                                     InterPro; IPR006209; E
InterPro; IPR003961; I
InterPro; IPR007110; I
InterPro; IPR007110; I
InterPro; IPR003598; I
InterPro; IPR008162; E
InterPro; IPR000436; S
InterPro; IPR0002035; V
                                            PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50853; FN3; 10.
PROSITE; PS50835; IG LIKE; 7
PROSITE; PS00387; PPASE; UNKO
PROSITE; PS50234; UWFA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Hypothetical protein K07E12.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acyltransferase; Complete SEQUENCE 749 AA; 84681
                                                                                                                                                                                                                                                                                                                                                                              investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
                       SEQUENCE
                                                                                                                                                                                                                                                                                                                              Ensembl; K07E12.1; Caenorhabditis elegans
WormBase; WBGene00019500; K07E12.1.
                                                                                                                                                                                                                                                                                                                                                        EMBL; U00054; AAM48546.1; HSSP; P01130; 1HZ8.
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Bristol
                                                                                                                                          SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORFNames=K07E12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8MQ08_CAEEL PRELIMINARY;
                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                    WormPep; K07E12.1b; CE31032.
                                                                                                                                                                                                                                                                                                                                                                                                     The C. elegans sequencing consortium; "Genome sequence of the nematode C. elegans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DBMQ08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                            n; PF00008; EGF; 1.
n; PF00041; fn3; 10.
n; PF00041; sushi; 1.
n; PF00084; Sushi; 1.
n; PF00092; VWA; 1.
vr; SM00032; CCF; 1.
vr; SM00181; EGF; 1.
vr; SM00181; EGF; 1.
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                                                                                                        SM00327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                  proteome;
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                        12268 AA;
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                                                                                                        VWA;
                                                                                                                   IGc2;
                                   Hypothetical protein
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FN III.
IEGF.
Ig-like.
Ig_c2.
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                                                                                                                                                                                                                                    Sughi
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  11.9%;
                        1282637 MW;
                                                         UNKNOWN_1.
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MW; 52E5AE51D0861002 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   -; Genomic_DNA.
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                                                                                                                                                                                                                                   SCR_CCP
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Pred. No.
  Score 83;
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                        4418C6C048E635A6 CRC64;
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81;
  BB
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  Length 12268;
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Q09165 CAEEL
ID Q09165 CAEEL
ID Q09165 CAEEL
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DT 01-MAR-2
DT 13-SEP-2
DT 01-MAR-2
DT 01-MAR-2
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DT 11-SEP-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proence R.B., Hedgecock E.M.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ
EMBL; U00054; AAA50715.2; -; Genomic DNA.
EMBL; AY117398; AAM78593.1; -; mRNA.
PIR; T16580; T16580.
HSSP; P01130; 1HZB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The C. elegans sequencing consortium; "Genome sequence of the nematode C. e investigating biology."; science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proenca R.B., Hedged
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein K07E12.1 (Mesocentin).
Name=dig-1, ORFNames=K07E12.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q09165 CAEEL PRELIMINARY;
Q09165; Q8MTB9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ensembl; K07E12.1; Caenorhabditis elegans
WormBase; WBGene00019500; K07E12.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30, GO:0005509, F:calcium
                                                                                                                                                                                                                                                                                                                                                                                            nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ormPep; K07E12.1a; CE32905
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                                                                                                                                SM000179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 PVSTTISKSFFAPEPRI--OPSFGENVGKEGALLFSVNLTVPENVSQVTVYPVYDEDYGL
                                                                                SM00408; IGc2; 1
SM00327; VWA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34,
PS00010; ASX HYDROXYL; 1
PS00196; COPPER_BLUE; UN
PS00022; EGF_1; UNKNOWN_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; IPR001881; EGF_Ca.; IPR006209; EGF_lik; IPR003961; FN_TII.; IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPLPTNDS---GHFV 10516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000152; Asx_hydroxyl_S: IPR000923; BlueCu_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WBGene00019500;
                                                                                                                                                                                                                                                                                                                                                                    IPR002035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003598;
                                                                                                                                8; EGF; 1.
1; fn3; 10.
1; fn3; 10.
7; 19; 3.
4; vwahi; 1.
32; CCCP; 1.
32; CCCP; 1.
60; FN3; 11.
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3; Mismatches 50;
                        UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 13100 AA
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Q6HQE5_BACAN
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Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                A Ritchcock P., Jackson P., Keim P., Longmire J., Lucas S., Ok.

A Richardson P., Rubin E., Tice H.;

"Complete genome sequence of Bacillus anthracis Sterne.";

Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AB017225; AAT57493.1; -; Genomic DNA.

GO; GO:0004239; F:methionyl aminopeptidase activity; IBA.

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0008233; F:peptidase activity; IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR001714; Pept M24 MAP.

R InterPro; IPR001714; Pept M24 MAP.

R InterPro; IPR0002467; Peptidase M24.

R PINTYS; PR001597; MAPEPTIDASE.

R PINTYS; PR005597; MAPEPTIDASE.

R PINTYS; PR005597; MAPEPTIDASE.

R PICKPAMS; TIGR00500; met pdase I; 1.

PROMESSON MAPEPTIDASE.

R PICKPAMS; TIGR00500; met pdase I; 1.

SEQUENCE 248 AA; 27062 MW; 14A6A817CE9BFD9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brettin T.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus cereus group.
NCBI_TaxID=1392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=BAS5204;
Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methionine aminopeptidase (MAP) (Peptidase M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6HQE5 BACAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sterne;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10446 PLGTDSSGSYITEDGQLVGKDEEGKPVGPDGQVL----PTDSAGHYVYPI----TGA 10494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10550 TPLPTNDS---GHFV 10561
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                                                  121 SPGIYNDQVMV-----
  75
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                                                                                                                                                                                                                23;
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PS01187; EGF_CA; 1.
PS50853; FN3; 11.
PS50835; IG_LIKE; 7.
                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                             LGRLVNTA-----DASQSIIYQIVDEKGKKMLKDHGAEVTPNQQITFKALNYTSGEKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPGIYNDQVMVGYYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DROILTTDAAGKPIYSVFNEDGIQLPTDSSGYAIGHDGELVPTESTNGVPLN-----KDG 10549
  AHGIPGDRVLKEGDLVNVDVSAALDGYYAD 104
                                                                                                        IGRIVALAREEMKKEAKPGMTTKELDLIGKKVLDEHGAISAPEKEYDPPGVTCISVNEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRLVNTADASQSIIYQIVDEKGKKMLKD-----HGAEVTFNQQITFKALNYTSGEKKI 120
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PS50234; VWFA; 4.
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                                                                                                                                                                                                                                         11.7%;
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25.2%; Pred. No.
cive 23; Mismato
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Last annotation updat
                                                                                                                                                                                                                                         Score 82;
Pred. No.
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                                                                                                                                                                                                                                            DB 2; Length 248 27;
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kinaka R.,
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C STRAIN-97-27;

C STRAIN-97-27;

A Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill A Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinak A Richardson P., Rubin E., Tice H.;

T "Complete genome sequence of Bacillus thuringiensis 97-27.";

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AED17355; AAT63446.1; -; Genomic DNA.

R EMBL; AED17355; AAT63446.1; -; Genomic DNA.

R GO; GO:0004239; F:methionyl aminopeptidase activity; IEA.

JR GO; GO:0008233; F:peptidase activity; IEA.

JR GO; GO:0008233; F:peptidase activity; IEA.

JR GO; GO:0008231; F:peptidase activity; IEA.
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EMBL; CP000001; AAU15226.1; -; Genomic DNA.

R GO; GO:0004239; F:methionyl aminopeptidase activity; IEA.

GO; GO:0006233; F:peptidase activity; IEA.

GO; GO:0006233; F:peptidase activity; IEA.

R GO; GO:0006508; P:proteojus and peptidolysis; IEA.

RR GO; GO:0006203; F:peptidase activity; IEA.

RR GO; GO:0006204; P:proteojus and peptidolysis; IEA.

RR GO; GO:0006204; P:proteojus and peptidolysis; IEA.

RR GO; GO:0006508; P:proteojus and peptidolysis; IEA.

RR GO; GO:0006204; P:peptidase AV24 MAP.

InterPro; IPR001714; Pept M24 MAP.

InterPro; IPR000994; Peptidase M24.

RR FEAm; PF00557; Peptidase M24; I.

RR PRINTS; PR00599; MAPEPTIDASE.

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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Methionine aminopeptidase (MAP) (Peptidase M).
Name=map; OrderedLocusNames=BT9727 5038;
Bacillus thuringiensis (subsp. konKukian).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
NCBI TaxID=180856;
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Bacillus cereus group.
NCBI_TaxID=288681;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillales; Bacillaceae; Bacillus
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hallacombe J.F., Gilna
Keim P., Longmire J.,
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as S., Okinaka
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Best Local
                                                                                                                                                                                                                                                       "Bacillus anthracis comparative genomics.";
submitted (MAY-2004) to the EMBL/GenBank/DDBJ
EMBL; AE017041; AAP29242.1; -; Genomic_DNA.
EMBL; AE017034; AAT34747.2; -; Genomic_DNA.
HSSP; P07906; 1C24.
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Ames / isolate 0581;
Ravel J., Rasko D.A., Shumway
Wilson M., Stanley S., Decker
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Methionine aminopeptidase (MAP) (Peptidase M).
Name=maP-3; OrderedLocusNames=BA5601, GBAA5601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000994; Péptidase_M24.
Pfam; PF00557; Peptidase_M24; I
PRINTS; PR00559; MAPEPTIDASE.
TIGRPAMS; TIGR00500; met pdase_I; 1.
Aminopeptidase; Cobalt; Complete proteome; Hydrolase; Protease.
SEQUENCE 248 AA; 27062 MW; 14A6A817CE9BFD9E CRC64;
                                                                                                                                                                                                               TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus cereus
NCBI_TaxID=1392;
                    GO; GO:0004239; F:methionyl aminopeptidase activity; GO; GO:0008233; F:peptidase activity; IEA. GO; GO:0006508; P:proteolysis and peptidolysis; IEA. InterPro; IPR001714; Pept_M24_MAP. InterPro; IPR002467; Pept_M24_MAP. InterPro; IPR002467; Pept_M24_MAP. InterPro; IPR002467; Pept_M24_M24. InterPro; IPR00294; Peptidase_M24. Pfam; PF00557; Peptidase_M24; I
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QB1JU4; Q6KJ8
                                                                                                                                                                                         TIGR;
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BACAN
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                                                                                                                                                                                         GBAA5601;
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25.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                      M.F., Jiang L.
S., Read T.D.,
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Salzberg S
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Search completed: April 10, 2006, 10:20:42 
Job time : 232 Becs
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              Rilstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
Popovic T., Fraser C.M.;
"Identification of anthrax toxin genes in a Bacillus cereus associated
with an illness resembling inhalation anthrax.";
Proc. Natl. Acad. Sci. U.S.A. 1018449-8454 (2004)
-1- CANTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shortgun (WGS) entry which is
preliminary data.
preliminary data.
Aminopeptidase; Hydrolase.
Aminopeptidase; Hydrolase.
Aminopeptidase; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Methionine aminopeptidase, type I (EC 3.4.11.18).
Name=map; ORFNames=BCE G9241 CNI_0258;
Bactllue cereus G9241.
Bacteria, Firmicutes; Bacillales; Bacillue cereus G9241.
Bactllue cereus group.
NCBI_TaxID=269801;
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STRAIN-G9241;
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Aminopeptidase; Cobalt; Complete proteome; Hydrolase; Protease.
SEQUENCE 264 AA; 28912 MW; AC21D93C604858DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D., Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W., Matden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z., Malden M.G.J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q4MGG1_BACCE PRELIMINARY;
Q4MGG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bMed=15155910; DOI=10.1073/pnas.0402414101;
                                                                                                                                                              121 SPGIYNDQVMV------GYYVN 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 AHGIPGDRVLKEGDLVNVDVSAALDGYYAD 124
                                                                                                                                                                                                                  35 IGRIVALAREEMKKEAKPGMTTKELDLIGKKVLDEHGAISAPEKEYDFPGVTCISVNEEV 94
                                                                                                                                                                                                                                                           67 LGRLVNTA-----DASQSIIYQIVDEKGKKMLKDHGAEVTPNQQITFKALNYTSGEKKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 AHGÍPGDRÝLKEGDLVNVDVSAALDGÝÝAD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 IGRIVALAREEMKKEAKPGMTTKELDLIGKKVLDEHGAISAPEKEYDFPGVTCISVNEEV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 LGRLVNTA-----DASQSIIYQIVDEKGKKMLKDHGAEVTFNQQITFKALNYTSGEKKI 120
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                                                                                                                                                                                                                                                                                                                    11.7%; Score 82; DB 2; Length 268; 25.6%; Pred. No. 30; tive 18; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.7%; Score 82; DB 2; Length 264; 25.6%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Run

OM protein -

protein search, using sw

mode1

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Result
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Maximum Match 10
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Perfect score:
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seq length: 2000000000
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Match Length
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699
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1: geneseqp198
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316.167 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
Listing
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                                                                                                                                                                                                                                                                                                                    geneseqp2005s:*
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geneseqp2001s:*
geneseqp2002s:*
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                           AAG10780
AEA36463
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ADW4795115
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AEB37679
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ADR14913
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ABP26319
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ADW47733
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                                                                                                                     Aeb40990
Abp26319
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Adc95115
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Adw47734
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Adw47737
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Adw47733 E. coli C
Adr14917 CS6 relat
                                                                                                                                        Aeb37679
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                                                                                                                                                                                                                                   Description
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E. coli C
          Bacterial
Lactobaci
                           L. pneumo
Bacterial
                                                                E. faeciu
Thermobif
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A. thalia
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Streptoco
Arabidops
                                                                                                                                                                                                       E. coli C
                                                      Staphyloc
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45	44	43	42	41	40	39	38	37	36	ω 5	ω 4	ω	32	31	30	29	28	27	26	25
72	72.5	72.5	72.5	72.5	73	73.5	73.5	73.5	74.5	74.5	74.5	74.5	75	75	75	75 .	75.5	75.5	75.5	75.5
10.3	10.4	10.4	10.4	10.4	10.4		10.5		10.7	10.7		10.7		10.7	10.7	10.7	10.8	10.8	٠	10.8
218	2541	1773	645	375	736	580	556	357	750	497	497	400	736	736	640	130	603	361	358	246
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ADA35599	AEB96985	ABB63908	ADY23668	ADA89505	AAU35880	ADN46850	ABU50258	ABU39054	ADB09635	ADS06735	ABP40269	AAG82840	ABU30700	AAU35700	ABU16767	ADH87135	ABM92198	ABB93393	AEA36477	ABU39391
Ada35599	Aeb96985	Abb63908	Ady23668	Ada89505	Aau35880	Adn46850	Abu50258	Abu39054	Adb09635	Ads06735	Abp40269	Aag82840	Abu30700	Aau35700	Abu16767	Adh87135	Abm92198	Abb93393	Aea36477	Abu39391
Acinetoba	BtD pepti	Drosophil	Plant ful	Staphyloc	Helicobac	Thermococ	Protein e	Protein e	Alloiococ	Staphyloc	Staphyloc	S. epider	Protein e	Helicobac	Protein e	Enterococ	M. xanthu	Herbicida	Cotton th	Protein e

ALIGNMENTS

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RESULT 1 ADR14916 13-MAY-1994;) 94US-00243482; 24-JAN-1997; 97US-00788145; 10-JAN-2000; 2000US-00479877 WPI; 2004-592722/57. Wolf MK, US2004156829-A1 Unidentified CS6; cssA; cssB; cssC; cssD; origin of replication; Lac promoter; kanamycin resistance gene; CS6A; CS6B; enterotoxigenic E. coli. CS6 related protein 04-NOV-2004 ADR14916; ADR14916 standard; protein; 136 02-FEB-2004; 2004US-00768093 12-AUG-2004. (USSA) US SEC OF ARMY. Cassels FJ, (first entry) Boedeker EC; ያ

The invention relates to a method of inducing, in a susceptible host, the production of antibodies against a CS6 protein, comprising administering a composition of matter comprising bacteria transformed with a plasmid containing genes cssA, cssB, cssC and cssB, an origin of replication, a Lac promoter and a kanamycin resistance gene, where the bacteria expresses both CS6A and CS6B proteins. The invention also relates to a composition of matter comprising a protein in a pharmaceutical carrier. The pharmaceutical carrier is a carbonated liquid. The method is useful for inducing the production of antibodies against the CS6 protein. The

Claim 4; SEQ ID NO 9;

22pp; English.

Inducing the production of antibodies against CS6 protein, useful for preventing pathological effects of enterotoxigenic E. coli, by administering a composition comprising transformed bacteria producing

CS6

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RESULT 2
ADW47737
Query Match
Best Local
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24-JAN-1997;
10-JAN-2000;
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effects
related
                     The invention relates to a method of inducing in a susceptible host, the production of antibodies against CS6 protein comprising giving a composition of matter made of bacteria transformed with a plasmid, which contain genes cssA and cssB, all of cssC and DNA sequence cssD that encodes at least 802 amino acids (at least 2406 base pairs), an origin of replication, a Lac promoter, and a kanamycin resistance gene, where the bacteria overexpress both CS6A and CS6B proteins. The method and proteins are useful for stimulating protective antibodies against enterotoxigenic Escherichia coli. This sequence corresponds to the E. coli CS6 ccsA
                                                                                                                                                                                                   Inducing in a susceptible host, the production of antibodies against CS6 protein, useful for stimulating protective antibodies against Escherichia coll by administering a composition comprising bacteria transformed with
                                                                                                                                                                                                                                                                                                                                                                                                                       12-JAN-2004; 2004US-00754641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E. coli CS6 ccsA mature protein
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                                                                                                                                                              Claim 4; SEQ ID NO
                                                                                                                                                                                        a plasmid.
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                                                                                                                                                                                                                                                                                     Wolf MK,
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                                                                                                                                                                                                                                                                                                                           (WOLF/) WOLF M K.
                                                                                                                                                                                                                                                                                                               (BOED/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                BOEDEKER E C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTEIATKNFPVSTTISKSFFAPEPRIQPSFGENVGKEGALLFSVNLTVPENVSQVTVYPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YDEDYGLGRLVNTADASQSIIYQIVDEKGKKMLKDHGAEVTPNQQITFKALNYTSGEKKI
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                                                                                                                                                                                                                                                                                    Cassels FJ,
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llarity 100.0%;
Conservative 0
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97US-00788145
2000US-00479877
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                                                                                                                                                                9;
                                                                                                                                                              23pp;
                                                                                                                                                                                                                                                                                      Boedeker EC;
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                                                                                                                                                                English.
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Pred. No. 1.1e-72;
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RESULT 3
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                    The invention relates to a method of inducing, in a susceptible host, the production of antibodies against a CS6 protein, comprising administering a composition of matter comprising bacteria transformed with a plasmid containing genes cssA, cssB, cssC and cssB, an origin of replication, a Lac promoter and a kanamycin resistance gene, where the bacteria expresses both CS6A and CS6B proteins. The invention also relates to a composition of matter comprising a protein in a pharmaceutical carrier. The pharmaceutical carrier is a carbonated liquid. The method is useful for inducing the production of antibodies against the CS6 protein. The protein and composition are used as vaccines for preventing pathological effects of enterotoxigenic E. coli. This sequence represents the Escherichia coli E8775 antigen cssA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CS6; cssA; cssB; cssC; cssD; origin of replication; Lac kanamycin resistance gene; CS6A; CS6B; enterotoxigenic Escherichia coli E8775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADR14912 standard; protein; 154
                                                                                                                                                                                                                               Inducing the production of antibodies against CS6 protein, useful for preventing pathological effects of enterotoxigenic E. coli, by administering a composition comprising transformed bacteria producing
                                                                                                                                                                                                                                                                                                                                                                                                       13-MAY-1994;
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                                                                                                                                                                                                                                                                                                   WPI; 2004-592722/57.
                                                                                                                                                                                                                                                                                                                                                                                           24-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2004156829-A1
                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                            Wolf MK,
                                                                                                                                                                                                                                                                                                                                                     (USSA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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97US-00788145.
2000US-00479877.
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                                                                                                                                                                                                                                                                                                                              Boedeker
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Pred. No. 1.1e-72
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                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                      Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c promoter;
E. coli;
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                                                                                                                                                                                                                                       CS6
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Sequence 154 AA,

Matches 136; Query Match Best Local

Similarity

100

.0%; Score

Conservative

0

Mismatches

e 699; DB 8; . No. 1.3e-72; smatches 0;

Length 154; Indels

0,

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RESULT 4
ADW47733
ID ADW4
   TRX SX EX BX PX AX
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The invention relates to a method of inducing in a susceptible host, the production of antibodies against CS6 protein comprising giving a composition of matter made of bacteria transformed with a plasmid, which contain gennes cssA and cssB, all of cssC and DNA sequence cssD that encodes at least 802 amino acids (at least 2406 base pairs), an origin of replication, a Lac promoter, and a kanamycin resistance gene, where the bacteria overexpress both CS6A and CS6B proteins. The method and proteins are useful for stimulating protective antibodies against enterocoxigenic Escherichia coli. This sequence corresponds to the E. coli CS6 ccsA
                                                                                                                                                                                                                      WPI; 2005-131784/14.
N-PSDB; ADW47732.
                                                                                                                                                                                                                                                           Wolf MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                        US2005025787-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E. coli CS6 ccsA full length protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADW47733 standard; protein;
                                                                                                                              Disclosure; SEQ ID
                                                                                                                                                                 Inducing in a susceptible host, the production of antibodies against CS6 protein, useful for stimulating protective antibodies against Escherichia coll by administering a composition comprising bacteria transformed with
                                                                                                                                                                                                                                                                                                                                                                                                              03-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Кеy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
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24-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                    12-JAN-2004; 2004US-00754641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibacterial; vaccine; DNA purification; colonization factor
                                                                                                                                                                                                                                                                                 (WOLF/) WOLF M K.
(CASS/) CASSELS F J.
(BOED/) BOEDEKER E C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                      10-JAN-2000;
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97US-00788145
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RESULT 5
ADRI4917
ADRI4917
ADRIA917
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24-JAN-1997; 97US-00788145.
10-JAN-2000; 2000US-00479877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resistance gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cassels FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cssB; cssC; cssD; origin of resistance gene; CS6A; CS6B;
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ilarity 100.0%;
Conservative
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Pred. No. 1.3e-72;
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enterotoxigenic
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Inducing the production of antibodies against CS6 protein, useful for preventing pathological effects of enterotoxigenic E. coli, by administering a composition comprising transformed bacteria producing CS6

Claim 6 SEQ ID NO 10; 22pp; English

The invention relates to a method of inducing, in a susceptible host, the production of antibodies against a CS6 protein, comprising administering a composition of matter comprising bacteria transformed with a plasmid containing genes cssA, cssB, cssC and cssD, an origin of replication, a Lac promoter and a kanamycin resistance gene, where the bacteria expresses both CS6A and CS6B proteins. The invention also relates to a composition of matter comprising a protein in a pharmaceutical carrier. The pharmaceutical carrier is a carbonated liquid. The method is useful for inducing the production of antibodies against the CS6 protein. The protein and composition are used as vaccines for preventing pathological effects of enterotoxigenic E. coli. This sequence represents a CS6 protein of

Sequence 146 AA,

Match

146;

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RESULT 6
ADR14913
ID ADR1
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Best Local
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                         production of antibodies against a CS6 protein, comprising administering a composition of matter comprising bacteria transformed with a plasmid containing genes casa, casa, casa and casa, an origin of replication, a Lac promoter and a kanamycin resistance gene, where the bacteria expresses both CS6A and CS6B proteins. The invention also relates to a composition of matter comprising a protein in a pharmaceutical carrier. The pharmaceutical carrier is a carbonated liquid. The method is useful for inducing the production of antibodies against the CS6 protein. The protein and composition are used as vaccines for preventing pathological effects of enterotoxigenic E. coli. This sequence represents the Escherichia coli E8775 antigen cssB of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ramamycin resistance gene; Escherichia coli E8775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                         Wolf
                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAY-1994; 94US-00243482.
24-JAN-1997; 97US-00788145.
10-JAN-2000; 2000US-00479877.
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kanamycin resistance ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli E8775
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                                                                                                                                                                                                   The invention
                                                                                                                                                                                                                                Disclosure; SEQ ID NO 6; 22pp; English.
                                                                                                                                                                                                                                                                                           preventing
                                                                                                                                                                                                                                                                                                            Inducing
                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                          Inducing the production of antibodies against CS6 protein, useful for preventing pathological effects of enterotoxigenic E. coli, by administering a composition comprising transformed bacteria producing
                                                                                                                                                                                                                                                                                                                                                                                                    (USSA ) US SEC OF ARMY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VYDEDYGLGRLVNTADASQSIIYQIVDEKGKKMLKDHGA-----EVTPNQQITF 108
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                                                                                                                                                                                                                                                                                                                                                                       Cassels FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                 relates to a method of inducing, in a susceptible host, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cssD; ori
ene; CS6A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen cssB protein.
                                                                                                                                                                                                                                                                                                                                                                         Boedeker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 113.5; DB 8;
Pred. No. 0.00014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        origin of
S6A; CS6B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replication; Lac enterotoxigenic E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         c promoter;
E. coli;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                                                                             producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
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Query Match

16.2%;

Score 113.5;

DB B --

Length 167;

Ś

KNFPVSTTISKSFFAPE----PRIQPSFGENVGKEGALLFSVNLTVPENVSQVTVYP---

Query Match Best Local : Matches

Local Similarity

16.2%; 28.5%;

Score 113.5; DB 9; Pred. No. 0.00017;

43;

Conservative

22;

Mismatches

55;

Indels Length

Gaps

59

167; 31,

Sequence 167 AA;

Sequence

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RESULT 7
ADW47734
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Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                           13-MAY-1994;
24-JAN-1997;
10-JAN-2000; 2
                                 The invention relates to a method of inducing in a susceptible host, the production of antibodies against CS6 protein comprising giving a composition of matter made of bacteria transformed with a plasmid, which contain genes cssA and cssB, all of cssC and DNA sequence cssD that encodes at least 802 amino acids (at least 2406 base pairs), an origin of replication, a Lac promoter, and a Kanamycin resistance gene, where the bacteria overexpress both CSGA and CSGB proteins. The method and proteins are useful for stimulating protective antibodies against enterotoxigenic Escherichia coli. This sequence corresponds to the E. coli CSG ccsB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADW47734
                                                                                                                                                                                                             Inducing in a susceptible host, the production of antibodies against CS6 protein, useful for stimulating protective antibodies against Escherichia coli by administering a composition comprising bacteria transformed with
                                                                                                                                                                                                                                                                                                                      (WOLF/)
(CASS/)
(BOED/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibacterial; vaccine; DNA purification; colonization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E. coli CS6 ccsB full length
                                                                                                                                                                                                  a plasmid.
                                                                                                                                                                                                                                                                    WPI; 2005-131784/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-2005
                          protein
                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                              Wolf MK,
                                                                                                                                                                                                                                                                                                                                                                                                                               12-JAN-2004; 2004US-00754641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2005025787-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
                                                                                                                                                                                                                                                                                                                      ) WOLF M K.
) CASSELS F J.
) BOEDEKER E C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAI-YTGGEYPNSGYSSGTYAGNLTVSFYSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KALNYTSGE---KKISPGIYNDQVMVGYYVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTSSGQQIGKLVNVNNPDQNMNYYI-----RKDSGAGNFMAGQKGSFPVKENTSYTF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYDEDYGLGRLVNTADASQSIIYQIVDEKGKKMLKDHGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSLDVNVNIEQNFI-PDIDSAVRIIPVNYDSDPKLDSQLYTVEMTIPAGVSAVKIAPTDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNFPVSTTISKSFFAPE----PRIQPSFGENVGKEGALLFSVNLTVPENVSQVTVYP---
                                                                                                                                                                                                                                                                                              Cassels FJ,
                                                                                                                                                                                                                                                                                                                                                                          ; 94US-00243482.
; 97US-00788145.
; 2000US-00479877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli.
                                                                                                                                                                          SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry
                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                         O
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                                                                                                                                                                       6; 23pp;
                                                                                                                                                                                                                                                                                                 Boedeker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   $
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ches 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -EVIPNOQITF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
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RESULT 8
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                                                        Query Match
Best Local S
Matches 35
                                                                                                                                                The present invention relates to Aspergillus fumigatus genes that are essential and are potential targets for drug screening. The methods and compositions of the present invention are useful for diagnosing and/or treating invasive Aspergillus fumigatus infection, including the allergic forms of the disease, such as Farmer's lung disease. They can also be used in various drug discovery purposes, such as expression of the recombinant protein, hybridization assay and construction of nucleic acid arrays. The present sequence represents an Aspergillus fumigatus essential gene protein sequence, used during diagnosis and drug development in the invention. These genes share a high degree of sequence conservation with known essential genes of candida albicans. The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug
                                                                                                                                                                                                                                                                                                                                                                                                      New purified or isolated Aspergillus fumigatus nucleic acid molecule encoding a gene product, useful for diagnosing and/or treating invastungal infections, such as Farmer's lung disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2003; 2003US-0441281P
13-JUN-2003; 2003US-0478196P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus fumigatus essential gene protein #465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADR86415 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 3465; 164pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADR85828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JAN-2004; 2004WO-US001099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004067709-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fungicide;
                                                                                                                      Sequence 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELIT-)
1031 ATTIVNRVQSPAAEANGTKAPSVEP---EGTAKERSARTLGLMNVPDTVNDARIRAMV-E 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2004-594200/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ecreening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 SAI-YTGGEYPNSGYSSGTYAGNLTVSFYSN 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                             12 STTISKSFFAP-----EPRIQPSFGENVGKEGALLFSVNLTVPENVSQVTVYPVYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELITRA PHARM INC.
ELITRA CANADA LTD.
                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYDEDYGLGRLVNTADASQSIIYQIVDEKGKKMLKDHGA-----EVTPNQQITF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTSSGQQIGKLVNVNNPDQNMNYYI-----RKDSGAGNFMAGQKGSFPVKENTSYTF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hu W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                      $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lemieux S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                          12.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fumigatus
                                                            20;
                                                            Score 84.5; D
Pred. No. 8;
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136
                                                                                           DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Farmer's
                                                            53;
                                                                                           Length 1239;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease;
                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                        invasive
                                                             Gaps
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RESULT 9
AEB37679
ID AEB3
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S
                             Query Match
Best Local S
Matches 29
                                                                                                                                   The invention relates to an isolated or purified nucleotide sequences (I) from Legionella pneumophila Paris strain. (I), and their related sequences or fragments, are useful as primers and probes for detection and amplification, including differentiation between the Paris and Philadelphia strains of Legionella pneumophila and to prepare recombinant (hybrid) polypeptides (II). (II) are also useful for preparation of specific antibodies (Ab), also used for detection/identification of Legionella, and some (I), specifically those involved in synthesis of surface proteins, are targets for identification of inhibitors. (II), or vectors that contain (I), are useful as vaccines and immunogenic compositions, for treatment and prevention of infections by L. pneumophila. The present squence represents the amino acid sequence of a
                                                                                                                                                                                                                                                                                                                                                              New genome of Legionella pneumophila Paris strain and derived polypeptides, useful for detection or identification of the s for treatment and prevention of infections.
                                                                                       Sequence 610 AA;
                                                                                                                                                                                                                                                                                                                                  Claim 3; SEQ ID NO 2011; 660pp; English.
                                                                                                                                                                                                                                                                                                                                                             polypeptides, useful for dete
for treatment and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-388305/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buchrieser C, Tichit
Rusniok C, Bouchier
Jarraud S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-2003; 2003FR-00013687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-SEP-2004; 2004WO-IB003578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Legionella pneumophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L. pneumophila protein SEQ ID NO 2011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEB37679 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INSP ) INST PASTEUR.
                                                                                                                   pneumophila protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1147 KGGPG 1151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 DYG-LGRLVNTADASQSII-YQIVDEKGKKMLKDHGAEVTPNQQI---TFKALNYTSGEK
    9 FPVST----
                               29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INSERM INST NAT SANTE & RECH MEDICALE. UNIV LYON 1 BERNARD CLAUDE. CNRS CENT NAT RECH SCI.
                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYGPLIKIVLRPDHQGAIVEFADVNHAGKASLELEGQETAPGORLHVGTVSELLKQSAEK 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KISPG
                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tichit M,
ouchier C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 610
    -----TISKSFFAPEPRIQPSFGENVGKEGALLFSVNLTVPENVS
                                             11.7%;
25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Etienne J, Ma L,
Zidane N, Magnier
                                19;
                                Score 81.5; I
Pred. No. 6.3;
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ጀ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cazalet C,
                                                           Length 610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glaser P;
Vandenesch
                                                                                                                                                                                                                                                                                                                                                                                   strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TJ
      53
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312 PPVSSDDFEAFREALAKLSLNDASLFYEPESSEALGFGFRCGFLGMLHMEI---IQERL-

54

QVTVYPVYDEDYGLGRLVNTADASQSIIYQIVDEKGKKMLKDHGAEVTPNQQI

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                                                                                                                                        XEXEGERATERXERXERXOSOSOSOSOSOS
                                                                                             Matches
                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      Buchrieser
Rusniok C,
Jarraud S;
                                                                                                                                                                      Philadelphia strains of Legionella pneumophila and to prepare recombinant (hybrid) polypeptides (II). (II) are also useful for preparation of specific antibodies (Ab), also used for detection/identification of Legionella, and some (I), specifically those involved in synthesis of surface proteins, are targets for identification of inhibitors. (II), or vectors that contain (I), are useful as vaccines and immunogenic compositions, for treatment and prevention of infections by L. pneumophila. The present squence represents the amino acid sequence of a
                                                                                                                                                                                                                                                                                                                                    New genome of Legionella pneumophila Paris strain and derived polypeptides, useful for detection or identification of the streatment and prevention of infections.
                                                                                                                                                            compositions, for treatment squence
                                                                                                                                                                                                                                                        rrom Legionella pneumophila Paris strain. (I), and their related sequences or fragments, are useful as primers and probes for detect and amplification, including differentiation between the Paris and amplification.
                                                                                                                                                                                                                                                                               The invention relates to an isolated or purified nucleotide sequences (I) from Legionella pneumophila Paris strain. (I), and their related
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-388305/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INSP )
(INRM )
(UYLY-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2005049642-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEB40990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEB40990 standard; protein; 610
                                                                                                                                      Sequence 610 AA;
                                                                                                                                                                                                                                                                                                                 Claim 3; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-NOV-2003; 2003FR-00013687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-SEP-2004; 2004WO-IB003578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Legionella pneumophila
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                                                                                                        Local
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INSERM INST NATE & RECH MEDICALE.
UNIV LYON 1 BERNARD CLAUDE.
CNRS CENT NAT RECH SCI.
                                                                                                      Similarity
                              QVTVYPVYDEDYGLGRLVNTADASQSIIYQIVDEKGKKMLKDHGAEVTPNQQI
                                                  PPVSSDDFEAFREALAKLSLNDASLFYEPESSEALGFGFRCGFLGMLHMEI---IQERL-
                                                                     FPVST------
                                                                                                                                                                                                                                                                                                                                                                                                         CC, LE Bouchier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection; Antibacterial; Vaccine.
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                   ID NO 5322;
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buchier C,
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         EREYNLD-LISTA---PTVVYQIVTQKGETLLIDNPSHLPPTPQI
                                                                                                        11.7%;
25.7%;
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Zidane N,
                                                                      ----TISKSFFAPEPRIOPSFGENVGKEGALLFSVNLTVPENVS
                                                                                                                                                                                                                                                                                                                 660pp; English.
                                                                                             19;
                                                                                            ; Score 81.5; DB
; Pred. No. 6.3;
19; Mismatches
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Magnier A,
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1, Kunst F,
                                                                                                                  Length 610;
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Vandenesch F;
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RESULT 11
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Best Local
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Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningits. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-352536/38.
N-PSDB; ABN66950.
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24-NOV-2000; 2000GB-00028727
07-MAR-2001; 2001GB-00005640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial;
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                                                                                                                                                                                                                                                                        Sequence 835 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a protein (ABP25413-ABP30895) from group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 3331; 4525pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-2001; 2001WO-GB004789
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(GENO-) INST GENOMIC RES
                                                           412
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72 NTADASOSIIYQIVDEKGKKMLKDHGAEVTPNQQITFKA-----LNYTSGEKKISPGI 124
                                                                                                                                                                l Similarity
29; Conserv
                                                           TPTLKTYTPAQPKVKP
                                                                                                             TTISKSFFAPEPRIQPSFGENVGKEGALLFSVNLTVPENVS-QVTVYPVYDEDYGLGRLV 71
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                                                                                                                                                                     Conservative
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                                                                                                                                                                                         11.4%; 21.8%;
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Pred.
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-DEAGQSV----NGKTVLPNAELNYVAKQDFSQYKGMTASQGKIAKNF

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RESULT 12
AAG10781
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                                            04-JUN-1999;
07-JUN-1999;
08-JUN-1999;
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14-MAY-1999
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14-MAY-1999
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19-MAY-1999
21-MAY-1999
24-MAY-1999
25-MAY-1999
25-MAY-1999
28-MAY-1999
28-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                  01-JUN-1999;
03-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                             EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
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29-MAR-1999
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99US-0131449P
99US-013240P
99US-0132485P
99US-01324867P
99US-0134256P
99US-01342518P
99US-01342118P
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99US-0126785P.
99US-0127462P.
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99US-0130510P
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8-0130077P.
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  27-JUL-1999;
28-JUL-1999;
02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
99US-0139454P

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99US-0139763P

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99US-0145918P

99US-0147308P

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99US-01488565P
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Query Match
Best Local S
Matches 33
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05-OCT-1999
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13-OCT-1999;
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20-SEP-1999;
22-SEP-1999;
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17-AUG-1999;
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                                                                                                                                  ch 11.2%; S
l Similarity 27.3%; P
33; Conservative 20;
ARVLAEGLNRIERLRVNVAAVETNIİYVDIPEDPKFGAEEACKSLEDVGVLVIP--QATF 304
                                                               PVGSVIVGSKKFITKARWLRKTLGGGMRQIGVLCAAALVALHENVAKL-----EDDHKK 246
                     -----GLGRL----VNTADASQSIIYQIVDEKGK------KMLKDHGAEVTPNQQITF 108
                                                                                                PVSTTI--SKSFFAPEPRIQPSFGENVGKEGALLFSVNLTVPENVSQVTVYPVYDEDY--
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99US-0155659P
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                                                                                                                                    Score 78.5; DB:
Pred. No. 5.7;
20; Mismatches :
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RESULT 13
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RESULT 14
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CC threonine aldolase, a mitochondrial targeting sequence, a 5 DNA promoter controlled and 3' terminator sequence, where the nucleic acid molecule, the mitochondrial targeting sequence, the promoter, and the terminator cc are operatively coupled to permit transcription of the nucleic acid molecule. This nucleic acid construct may be used in the generation of conscious and the terminator cc molecule. This nucleic acid construct may be used in the generation of conscious and the mitochondrial targeting sequence comprises a mitochondrial targeting sequence comprises a constituction and transcription of cold molecule may comprise a dominant negative mutation and encode a constructional threonine aldolase, resulting in suppression or interference of endogenous mRNA encoding threonine aldolase. The nucleic acid molecule is positioned in the nucleic acid construct to result in compression or interference of endogenous mRNA encoding threonine aldolase and be in the sense orientation, or the nucleic acid molecule is an antisense cform or a threonine aldolase conditions to a threonine aldolase and incording threonine aldolase and be caused by a chemical mutagenizing agent, e.g. or ethylmethanseulfonate, radiation, e.g. ultraviolet rays, gamma rays, or conditions to inactivate the gene, where the deactivating nucleic acid molecule into conditions to inactivate the gene, where the deactivating nucleic acid conditions acid molecule acid molecule acid molecule is a transposon, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid construct comprising a nucleic acid molecule, mitochondrial targeting, promoter, and terminator sequences, useful increasing threonine content in plant seeds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    configured to silence threonine aldolase expression or encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an example of a threonine aldolase which may be silenced by the nucleic acid molecule
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Query Match
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	45	44	43	42	41	40	39	38	37	36	ω	34	ω ω	32	Ω	30	
	70	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	71	71	71.5	
	10.0	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.2	10.2	10.2	
	242	2911	2366	1644	896	498	458	430	430	357	323	250	217	1157	318	812	
	N	N	N	N	N	N	N	N	N	ب	N	N	N	N	N	N	
	H82720	T20566	S10317	AC0823	AB1156	C90413	F84157	AH1750	AG1381	G64053	S69647	F72247	T29388	F97255	T50039	T01618	
_	outer membrane pro	hypothetical prote	toxin B - Clostrid	probable lipoprote	conserved membrane	dihydropteroate sy	thiophen and furan	enolase homolog en	enolase homolog en	chorismate synthas	hypothetical prote	methionine aminope	hypothetical prote	fusion of alpha-gl	beta-1,4-galactosy	hypothetical prote	

RESULT 1

ALIGNMENTS

CS6 structural subunit A - Escherichia coli C;Species: Escherichia coli C;Species: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change C;Accession: I60266 C;Accession: I60266 8 밁 5 밁 S A; Title: Cloning of genes encoding coli-surface (CS) A; Reference number: I60266 R; Willshaw, G.A.; Smith, H.R.; MCCO FEMS Microbiol. Lett. 49, 473-478, 吊 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-154 <RES> A;Cross-references: A; Accession: I60266 Query Match Best Local Matches 121/ 125; 79 61 YDEDYGLGRLVNTAÞASÖSIIYQIVDEKÁKKMLKDHGAEVTPNQQI 19 RTELATKNEPVSTTISKSFFAPBPQIDPSFCKWOGKEGGLLFGVSLTVPENVSQVTVY 1 RTEIATKNFPVSTTISKSFFAPFPR\QPSFGEN\GKEGALLF\$VNLSVPENVSQVTVYPV Similarity APGIYNDQVMVGYYVN 136 PAGIYNDQVMVGYYVN 154 YDEDYGLGRLVNTADDSGSIIYQIVDDI Conservative Smith, H.R.; McConnell, M.M.; UNIPROT: P53508; UNIPARC: UPI000012A400; EMBL: U04844; NID: g442375; æ ~: Score 655; DB 2; Pred. No. 1.4e-54; Mismatches GRKMIKDHGAEVTPNQQI1 Rowe, Length 154; antigens W Indels ij 09-Jul-2004 0 enterotoxigenic Escheric Gaps PV 78 60 0 PID

A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-167 <RES>

A;Cross-references: UNIPROT:P53510; UNIPARC:UPI000012A402; EMBL:U04844;

Query Match Best Local S Matches 43

Local Similarity 30.: tes 43; Conservative

17.2%; 30.1%;

Score 120.5; DB 2; Pred. No. 0.00041;

Indels

15;

Gaps

7;

Length 167;

NID: 9442375;

PID

C;Accession: I83348
R;Willshaw, G.A.; Smith, H.R.; McConnell, M.M.; Rowe, FEMS Microbiol. Lett. 49, 473-478, 1988
A;Title: Cloning of genes encoding coll-surface (CS) a;Reference number: 160266
A;Reference number: 160266

B. . antigens

ä

enterotoxigenic

CS6 structural subunit B - Escherichia coli C;Species: Escherichia coli C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004

RESULT 183348

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hypothetical protein all233 [imported] - Nostoc sp. (strain PCC 7120)
A;Note: Nostoc sp. Errain PCC 7120
A;Note: Nostoc sp. Etrain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Uul-2004
C;Accession: AF2097
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-13055 <FUL>
A; Cross-references: UNIPROT:Q09165; UNIPARC:UPI000017CF3A; EMBL:U00054; NID:g485140; A; Experimental source: strain Bristol N2
C; Genetics:
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A;Introne: 46/3; 85/2; 201/1; 278/2; 470/2; 817/1; 927/1; 960/3; 1265/1; 1322/1; 1478/3; 6014/3; 6159/3; 6665/2; 7266/3; 7895/3; 8669/3; 8726/3; 9803/3; 10937/3; 12234/2; 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein K07E12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16580
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A;Accession: T16580
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                                                                                                                                Status: preliminary
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRQILTTDAAGKPIYSVFNEDGIQLPTDSSGYAIGHDGELVPTESTNGVPLN-----KDG 10504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRLVNTADASQSIIYQIVDEKGKKMLKD------HGAEVTPNQQITFKALNYTSGEKKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLGTDSSGSYITEDGQLVGKDEEGKPVGPDGQVL----PTDSAGHYVYPI----TGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVSTTISKSFFAPEPRI--QPSFGENVGKEGALLFSVNLTVPENVSQVTVYPVYDEDYGL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYDEDYGLGRLVNTADASQSIIYQIVDEK--GKKMLKDHGA-EVTPNQQITFKALNYTSG 116 : | | | | | | | | | | | | | | | | |
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25.2%; Pred. No. 3.5e+02;
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                                                                      PIDN:BAB74032.1
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                                                                                                                                                 C:Acce88101: VVVIII R; Weidner, G.; Sawers, G.
J. Bacteriol. 178, 2440-2444, 1996
A;Title: Molecular characterization of the
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A; Molecule type: I A: Residues: 1-740

protein 0 <WEI2>

UNIPARC: UPI0000131758

A; Accession: PC6004

A; Cross-references: UNIPROT: Q46266; UNIPARC: UPI0000131758;

EMBL: X93463; NID: g1072360;

ВÌ

genes encoding pyruvate formate-lyase PMID:8636053

A; Molecule type: DNA A; Residues: 1-740 <WEI1> A; Reference number: JC6010; A; Accession: JC6010

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R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: A81293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable flagellar hook-associated protein Cj1466 [imported] - Campylobacte
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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            formate C-acetyltransferase (EC 2.3.1.54) - Clostridium pasteurianum N;Alternate names: Pf1 protein; pyruvate formate-lyase C;Species: Clostridium pasteurianum C;Species: Clostridium pasteurianum C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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Accession: JC6010; PC6004
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Best Local :
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Best Local
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                                                                                                                                                                                                                ISPGIYNDQVMVGY 133
                                                                                                                                                                                                                                                                                         EDYGLGRLVNTADASQSIIYQIVDEKGKKMLKDHGAEVTPNQ---QITFKALNYTSGEKK 119
                                                                                                                                                                                                                                                                                                                             VSAVASKNEINODNRLDTTITDPGHQYNLSIEG---FSI-----VDGINFHPLKLDYD
                                                                                                                                                                                                                                                                                                                                                                    VSTTISKSFFAPEPRI-----QPSFGENVGKEGALLFSVNLTVPENVSQVTVYPV---YD
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Pred. No.
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Pred. No. 11;
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, S.; Barrel
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R;Kuroda, W; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1255-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     formate acetyltransferase [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C;Accession: E89785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
E89785
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C; Superfamily:
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A,Rasidues: 1-749 <KUR>
A,Cross-references: UNIPROT:Q99WZ7; UNIPARC:UPI00000D789B; GB:BA000018; PID:g13700141;
A,Experimental source: strain N315
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                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 40
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Best Local S
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                                                                                                                                                                          344 LVTKNSFRFLHSLDNLGPAPEPNL------TVLWSVRL--PDNFKTYCAKMSIK 389
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39; Conservative
                                                                                                                                                                                                                                                                                    Similarity
                                                                                  TSSIQYENDDIMRESYGDDYGIACCVSAMTIGKQMQFFGARANLAKTLLYAINGGKDEK- 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-QQITFKALNYTSGEKKISPGIYND-QVMVGYYVN 136
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                                    LKDHGAEVTPN-QQITFKALNYTSGEKKISPGIYNDQVM----VGYYVN 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                formate C-acetyltransferase 1; glycyl radical homology
                                                                                                                                 -----SQVTVYPVYDEDYGLGRLVNT---
-SGAQVGPNFEGINSEVLEYDEVFKKF---
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                                                                                                                                                                                                                                                                                  11.1%; Score 77.5;
23.8%; Pred. No. 31
                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                  Mismatches
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-DOMMOWLAGVYIN
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                                                                                                                              ADASQSIIYQIVDEKGKKM 92
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RESULT 8

RESULT

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A;Residues: 1-4936 <KUR>
A;Cross-references: UNIPROT:Q8YKJ3; UNIPARC:UPI000011021D; GB:BA000020; PIDN:BAB78388.1;
A;Experimental source: strain PCC 7120
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A;Note: Nostoc sp. Strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH5515
C;Accession: AH5515
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
                                                                                                                                                                                                                                                                                                                         A;Map position: 3
A;Introns: 86/2; 118/2; 164/1; 233/1; 280/2; 322/2
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: T25354
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-356 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, February A; Reference number: Z20021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T27D1.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: alr7304
                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: CESP:T27D1.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: clone
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Experimental source: clone T27D1
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Best Local (
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342
                                                      110 ALMYTS 115
                                                                                                         282 VLNVTIHPPYDFILLMNALAMTCSASNPLLYTLFSQKFRRRLRDVLYCPSDVENETKTYY 341
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                                                                                                                                                                                                                                               Similarity
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SINNTS
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                                                                                                                                                            VSQVTVYPVYDEDYGLGRLVNTADASQSIIYQIVDEKGKKMLKD--HGAEVTPNQQITFK 109
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347
                                                                                                                                                                                                                  11.0%; Score 77; DB 28.8%; Pred. No. 14; ative 15; Mismatches
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                                                                                                                                                                                                                                                                         DB 2;
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C;Accession: F69481

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fletschmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370; 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A; Reference number: A69250; MUID: 98049343; PMID: 9389475

A;Accession: F69481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable acid-CoA ligase (EC 6.2.1.-) - Archaeoglobus fulgidus
C,Species: Archaeoglobus fulgidus
C,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Molecule type: CANDA
A;Residues: 1-569 <WIL>
A;Cross-references: UNIPARC:UPI000007FD46; EMBL:Z78198; PIDN:CAB01568.1; GSPDB:GN00023;
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A,Residues: 1-557 <KLE>
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A;Accession: T22711
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A, Residues: 1-569 <WAN>
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;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004;Accession: T43531; T22711
                                                                                                                                                                                                                                                                                                                         Cross-references: UNIPROT:O28423; UNIPARC:UPI0000056B85; GB:AE000975; GB:AE000782; NIE;Superfamily: probable acyl-CoA ligase medium chain; acetate-CoA ligase homology;Keywords: acid-thiol ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: T43531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: F55C5.3
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                                                                                                                                                                                 Matchee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                 -546/Domain: acetate-CoA ligase homology <ACL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            523
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;
                                                                                                                  4 IATKNEPVSTTIS---KSFFA----PEP-----RIQPS--FGENVGKEGALLFSV 44
                                                                                                                                                                                                h 10.9%; Score 76; DB Similarity 27.2%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 10.9%; Score 76.5; DB 2; Similarity 30.8%; Pred. No. 27; 20; Conservative 12; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TMSIVEDEEEGVKRLIQSQSLEDRIIFLFVDEHKKSMLKERITQTYPS-----KADKYVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGQRV 527
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      NLTVPENVSQVTVYPVYDEDYGLGRLVNTADASQSIIYQIVDEKGKKMLKDHGA 98
                                                           VAILKHPMASQLSFDKLKYFAQGSAPPPPWTFVELKNRGIEPMNIWGQN---EGTGLFSY 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140/1; 171/2; 294/2; 338/3; 382/2; 508/2
                                                                                                                                                                                 Conservative
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                                                                                                                                                                                 22; Mismatches
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                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                 31; Indels
                                                                                                                                                                                                                                     Length 557;
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A;Experimental source: strain 9a5c

A;Experimental source: strain 9a5c

R;Simpson, A,J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Br. Poccena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrenado, M.A.; Madeira, H.M.; Maxino, C.L.; Marques, M.V.; Maxrins, E. A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.J., da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chaperone protein precursor XF0082 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa (C;Species: Xylella fastidiosa (C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pectin methyl-esterase-like protein - Arabidopsis
N;Alternate names: protein TZII.140
C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-266 <SIM>
A;Cross-references: UNIPROT:Q9PH64; UNIPARC:UPI00000C22C4; GB:AE003862; GB:AE003849; NII
A;Cross-references: UNIPROT:Q9PH64; UNIPARC:UPI00000C22C4; GB:AE003862; GB:AE003849; NII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
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C; Accession: T49882
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                                                                      C; Genetics:
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A; Introns: 68/3; 161/3; 229/3; 309/2
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A;Experimental source: cultivar Columbia; BAC clone T2I1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: Z24493
A; Accession: T49882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: A82851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
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;Gene: XF0082
;Superfamily: chaperone protein papD
                                                                                                       Contents: annotation
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Pred. No. 19;
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A,Moleccie type: DNA
A,Residues: 1-1472 <SIM>
A,Residues: 1-1472 <SIM>
A,Cross-references: UNIPROT:Q9PG24; UNIPARC:UPI00000C2413; GB:AE003897; GB:AE003849; NII
A,Cross-references: UNIPROT:Q9PG24; UNIPARC:UPI00000C2413; GB:AE003897; GB:AE003849; NII
A,Experimental source: Strain 9a5c
A,Experimental source: Strain 9a5c
A,Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Camargo, M.F.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, I
Briones, M.R.S.; Bueno, M.R.D.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, I
as-Neto, E; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
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R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: D64534
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C;Date: 09-Aug_1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
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R;annonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                              ),Note: for a complete list of authors see reference number A59328 below
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                                                                                                                                                                                                                                                                                                                                                                              Status: preliminary
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htive 29; Mismatches
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Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohmr, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.B.; Laigu
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A;Gene: XF0478
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                                                     KMLKDHGAEVTPNQQITFKALNYTSGEKKI 120
                                                                                                                  AIAKRVIYT---ALSHVDDTNRA--SVVRRFVAEKLVESSSGDVATDAAQVFGRFGYTPR 900
                                                                                                                                                                    QVTVYPVYDEDYGLGRLVNTADASQSIIYQIVDEK-----
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Search completed: April 10, 2006, 10:21:26 Job time : 40 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-134-000C-5001
US-09-134-001C-5114
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US-09-134-000C-6740
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US-09-134-000C-6740
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Sequence 4742, Appl
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RESULT 2 US-09-107-53; Sequence 47; Patent No.; GENERAL 1 APPI; INUME NUME CORE	3 00	RESULT 1 US-09-248-7 US-09-248-7 Sequence Patent No GENERAL II APPLICAN TITLE OF FILE REF CURRENT CURRENT CURRENT PRIOR AP PRIOR AP PRIOR FI PRIOR FI PRIOR FI INUMBER OF LENGTH: TYPE: P ORGANIS US-09-248-7	44443333333333333333333333333333333333
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143 DDQVSDVIKYGQSNGWD 143 DDQVSDVIKYGQSNGWD 532A-4742 4742, Application US 0. 6583275 L INFORMATION: LYIN A DOUC PPLICANT: LYIN A DOUC PPLICANT: LYIN A DOUC PRICE OF INVENTION: NU ITLE OF SEQUENCES: 7 DRRESPONDENCE ADDRESS ADDRESSEE: GENOME	imilarity 22.2 ; Conservative ; Conservative STTISKSFFAPERIQ [: : SSTSSTSTESPSP SSTSSTSTESPSP STADASOSITYQIVDE : : : KSADTIRSDI-QLINS EKKISP	I-796A-14853 NO. 6747137 NO. 6747137 INFORMATION: WICKLEIC OF INVENTION: WUCLEIC OF INVENTION: FOR DIA EFFERNCE: 107196.132 FILING DATE: 1999-0 APPLICATION NUMBER: US FILING DATE: 1999-02-1 APPLICATION NUMBER: US FILING DATE: 1998-08-1	9.9 660 9.9 1319 9.9 1319 9.9 350 9.9 350 9.8 197 9.8 229 9.8 548 9.8 616 9.7 356
DDQVSDVIKYGQSNGWDVFNLLTICNEAIIAGY DDQVSDVIKYGQSNGWDVFNLLTICNEAIIAGY 2, Application US/09107532A 583275 FORMATION: CANT: Lynn A Doucette-Stamm and COF INVENTION: NUCLEIC ACID AND A ENTEROCOCCUS FAECI R OF SEQUENCES: 7310 SPONDENCE ADDRESS: GENOME THERAPEUTICS CO	imilarity 22.2%; Pred. No; Conservative 23; Misma; STTISKSFFAPEPRIQPSFGENVGKEGA;	US/09248 et al ACID AN AGNOSTIC US/09/2 02-12 02-12 06/074 13 60/096	2 US-09- 2 US-09-
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US-09-323-872A-25
; Sequence 25, Application US/09323872A
; Patent No. 6395539
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LOCATION: (B) LOCATION 1...378
SEQUENCE DESCRIPTION: SEQ ID NO: 4742:
US-09-107-532A-4742
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                   PRIOR APPLICATION NUMBER: 09/072,433
PRIOR FILING DATE: 1998-05-04
NUMBER OF SEQ ID NOS: 58
                                                                                                       APPLICANT: Coschigano, Peter
TITLE OF INVENTION: Compositions and Methods for Bioremediation
FILE REFERENCE: OHU-03640
CURRENT APPLICATION NUMBER: US/09/323,872A
CURRENT FILING DATE: 2001-06-15
                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4742:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
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MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                  292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 DLFAIDEPVEMFGLGRV----GELPQEIFIEAFVEQVKEAFQLDGLRIVQFKNAKSSVKRI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 TSIGHGRFTPEAGAQPAIGK-VGKTEQVQEAKVEVILPETIEKQVIQAMRSAHPYEEPAY 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTISKSFFAPEPRIOPSFGENVGK-EGALLFSVNLTVPENVSQVTVY------PVY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 378 amino acids TYPE: amino acid
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TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 30
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not rel
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OH
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                             Local Similarity
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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395 PIYGDDYAIACCVSAMRVGKDMQFFGARCNLAKCLLLAINGGVDEK------KGIKVVP 447
                                                                               336 LVTKNSFRYLHTLINLGSÅPEPNMTVLWSENL-PESFKKFCAEMSILTDSIQYENDDIMR 394
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                                     59 PVYDEDYGL--
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                                                                                                                  4 IATKN-FPVSTTISKSFFAPEPRIQPSFGENVGKEGALLFSVNLTVPENVSQV----TVY 58
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California
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220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                       740 amino acids
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25.0%; Pred. No. 2.1;
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                                                                                                                                                          22; Mismatches
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                                       GRLVNTADASQSIIYQIVDEKGKKMLKDHGAEVTP 102
                                                                                                                                                                                                  DB 2;
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                                                                                      Matches
                                                                                                           Query Match
Best Local
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SEQ ID NO 11397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT: GARY BRETON
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
BILE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
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TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/217,883 PRIOR FILING DATE: 2000-07-10
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                                                                                                                                                                                                                            LENGTH: 603
TYPE: PRT
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                                                                                      n 10.8%; Score 75.5; DB 2;
Similarity 26.5%; Pred. No. 2.7;
30; Conservative 17; Mismatches 35.
PPVDSADYENLRDALAKLVLNDSAPTYEPESSTALGPGPRCGYLGLLHMEI --- VQERL- 359
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                                       FPVST-----TISKSFFAPEPRIOPS--FGENVGKEGALLFSVNLTVPENVS 53
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                                                                                           Indels
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US-09-134-000C-5020
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                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
SEQ ID NO 5020
LENGTH: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: LYMN DOUCETTE-Stamm et al
APPLICANT: INVENTION: NUCLEIC ACID AND AMINO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS
FILE REFERENCE: 032796-032
CURRENT APPLICATION UNMERR: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2774, App
Patent No. 6703492
                                                                                                                                                      Matches
                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: PU3480US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 6812
                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                               ENGTH:
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                                                                                                                                                                                                                                                                                                                                               400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
25; Conserv
                                                                                                                                                      38;
                                                                                                              8 NFPVSTTISKSFFAPEPRIQPSFGENVGK------EGALLFSVNLTVPEN 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARNSNYOPTFONVNSVNGADDISP 103
VMNGYLYPKYLKDTFDNDGYFQTGDIABIDDEGYVIIY----DRRKDLIISGGENIYP-Y 307
                                  VSQVTVYPVYDED-----YGLGRLVNTADASQSIIYQIVDEKGKKMLKDHGAEVTPNQ 104
                                                                          SFGMTETCSQ-FLTASPOMLKERFDTVGKPSENVEVKIKNPNAYGHGELLIK-----GEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVTVYPVYDEDYGLGRLVNTADASQSIIYQIVDEKGKKMLKDHGAEVTPNQQI 106
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09710279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                      10.7%;
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                                                                                                                                                      21; Mismatches
                                                                                                                                                                      Score 74.5; DI
Pred. No. 1.9;
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Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                              DB*2;
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                                                                                                                                                                                            Length 400;
                                                                                                                                                        Indels 37;
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RESULT 10
US-09-248-796A-17536
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                                                                                                                                                       ) ORGANISM: Candida albicane
US-09-248-796A-17536
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                SEQ ID NO 17536
LENGTH: 467
TYPE: PRT
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                                                                 Matches
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Patent No. 6747137
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                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/074,725 PRIOR FILING DATE: 1998-02-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h . 10.7%; Score 74.5; D
Similarity 24.7%; Pred. No. 2.7;
                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QITFKALNYTSGEKKISPGIYND---QVMVGYYV 135
ATKNFPVSTTISKSFFAPEPRIQPSFGENVGKEGALLFSVNLTVPENVSQVTVYPVYDED 64
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                                                                 Conservative
                                                                                     10.6%; Score 74; 25.7%; Pred. No.
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                                                                 Mismatches
                                                                                     DB 2; Length 467
2.8;
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                                                                                                                                                ; ORGANISM: Human US-09-949-016-6079
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US-09-949-016-6079
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US-09-328-352-6886
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6886
LENGTH: 218
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6079
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Patent No. 681233
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GENERAL INFORMATION:
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                                                                    Matches
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 LNYYAEYYATGAS--TAGTVTSOV 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 LVTDNTCTIDTGDKNLTVNLPTVSSQSLKNAGDVAGRTPFQINLTNCASVGKVATYFEPG 129
                                                                                                                                                                                                                    1005
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                                                                    Similarity
21; Conser
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RTEIATKNFPVSTTISKSFFAPEPRIQPSFGENVGKEGALLFSVNLTVPENVSQVT 56
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                                                                                      10.3%;
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                                                                  Score 72; DB 2;
Pred. No. 16;
8; Mismatches 2
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                                                                                                            Length 1005;
                                                                      Indels
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RESULT 14
US-09-134-000C-6740
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US-09-949-016-7359
                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6740, Application US/09134000C Patent No. 6617156 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
SEQ ID NO 6740
LENGTH: 1467
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                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lynn Doucette-Stamm et al MITICE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTENCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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Local Similarity 25.2%; Pred. No. 33;
hes 33; Conservative 21; Mismatches
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Local Similarity 37.5%;
nes 21; Conservative
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                                                                                                                                                                 835 KIEESFTEEINKE--VEKTINTVVEEQIEKVEEKKKKTTEDDVRDHLRGFARTIPAFLMA 892
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KVIPGLFNEVV 950
                                     KISPGIYNDOV 129
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; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YDR480W
US-09-538-092-213
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SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 213
LENGTH: 323
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                                                                                                                                                                             Matches
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CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
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IITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                      y Match 10.1%; Score 70.5; D
Local Similarity 24.7%; Pred. No. 4.4;
hes 23; Conservative 21; Mismatches
                                                                                                                            49 PENVSQ---VTVYPVYDEDYGLGRLVNTADASQSIIYQIVDEKGKKML------KDHG 97
76
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  GKPPTITTSPAEKTVPFKSLNHSLKRKRVPPAL 108
                                    AE----VTPNQQ-ITFKALNYTSGEKKISPGI 124
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Search completed: April 10, 2006, 10:22:19
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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342.318 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-267-989-25
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		33, Ap 3397, Ap 3992, A Appli 3550, 3566, A 448, A 1174, 448, A 1174, Appli 361, A 361, A 361, A 361, A 361, A

Query Match Best Local Similarity

100.0%;

Score 699; DB 4; Pred. No. 5e-67;

Length 136;

CITY: Fairfax

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; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-754-641-9
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Publication No. US20040156829A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-01-24
PRIOR APPLICATION NUMBER: 08/243,482
PRIOR FILING DATE: 1994-05-13
NUMBER OF SEQ ID NOS: 9
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PRIOR FILING DATE: 2000-01-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITLE OF INVENTION: TRANSFORMED BACTERIA PRODUCING CS6 ANTIGENS AS ILE REFERENCE: 034047.033.3 URRENT APPLICATION NUMBER: US/10/754,641 URRENT FILING DATE: 2004-01-12
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                                                        NUMBER OF SEQUENCES: 10
                                                                           Boedeker, Edgar C
TITLE OF INVENTION: Transformed Bacteria Producing GS6
Antigens as Vaccines
                                                                                                                                                        APPLICANT: Wolf, Marcia K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136;
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Boedeker, Edgar C.
ADDRESSEE: Hendricks and Assoc
STREET: P.O. Box 2509
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Pred. No. 5e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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US-10-768-093-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                  PRIOR APPLICATION NUMBER: 09/479,877
PRIOR FILING DATE: 2000-01-10
PRIOR PPLICATION NUMBER: 08/788,145
PRIOR FILING DATE: 1997-01-24
PRIOR PRIOR APPLICATION NUMBER: 08/243,482
PRIOR FILING DATE: 1994-05-13
                                                                                                                                                                     FILE REFERENCE: 034047.033.3
CURRENT APPLICATION NUMBER: US/10/754,641
CURRENT FILING DATE: 2004-01-12
                  NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                      APPLICANT: U.S. Army Medical Research and Materiel Command APPLICANT: Wolf, Marcia K.
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                                                                                                                                                                                                                                    PPLICANT: Cassels, Frederick J.
PPLICANT: Boedeker, Edgar C.
TLE OF INVENTION: TRANSFORMED BACTERIA PRODUCING CS6 ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/479,877B
FILING DATE: 10-Jan-2000
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna M
REGISTRATION NUMBER: 32,535
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/425-8405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139
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PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDEDYGLGRLVNTADASOSIIYQIVDEKGKKMLKDHGAEVTPNQQITFKALNYTSGEKKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTEIATKNFPVSTTISKSFFAPEPRIQPSFGENVGKEGALLFSVNLTVPENVSQVTVYPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 22031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 154 amino acids
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100.0%; Pred. No. 6
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TYPE: PRT
; ORGANISM: Escherichia coli
US-10-754-641-5
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Publication No. US20040156829A1
GENERAL INFORMATION:
APPLICANT: Wolf, Marcia K
Query Match 16.2%; Score 113.5; DB 4; Best Local Similarity 28.5%; Pred. No. 0.00061; Matches 43; Conservative 22; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/768,093
FILLING DATE: 02-Feb-2004
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                             TOPOLOGY: unknown MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/479,877B
FILING DATE: 10-Jan-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                NAME: Hendricks, Glenna M
REGISTRATION NUMBER: 32,535
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/425-8405
TELEPAX: 703/425-8406
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Antigens as Vaccines
                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTEIATKNFPVSTTISKSFFAPEPRIQPSFGENVGKEGALLFSVNLTVPENVSQVTVYPV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Hendricks and Assoc
STREET: P.O. Box 2509
CITY: Fairfax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDEDYGLGRLVNTADASQSIIYQIVDEKGKKMLKDHGAEVTPNQQITFKALNYTSGEKKI 138
                                                                                                                                                                                                                       LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: VA
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Boedeker, Edgar C
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                                         Length
    Indels
    31;
    Gaps
    7;
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Publication No. US20040156829A1
GENERAL INFORMATION:
APPLICANT: Wolf, Marcia K
                                                                                                                                           Matches
                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                           NAME: Hendricks, Glenna M
REGISTRATION NUMBER: 32,535
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/425-8405
TELEFAX: 703/425-8406
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cassels, Fred J
Boedeker, Edgar C
TITLE OF INVENTION: Transformed Bacteria Producing GS6
Antigens as Vaccines
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                                 60 VYDEDYGLGRLVNTADASQSIIYQIVDEKGKKWLKDHGA-----EVTPNQQITF 108
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86 LTSSGQQIGKLVNVNNPDQNMNYYI---
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                                                                                                         7 KNFPVSTTISKSFFAPE----PRIQPSFGENVGKEGALLFSVNLTVPENVSQVTVYP--- 59
                                                                                                                                             43;
                                                                                                                                                              Similarity
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                                                                     KSLDVNVNIEQNFI-PDIDSAVRIIPVNYDSDPKLDSQLYTVEMTIPAGVSAVKIAPTDS 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KALNYTSGE---KKISPGIYNDQVMVGYYVN 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                            ENGTH: 167 amino acids
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                                                                                                                                             Conservative
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                                                                                                                                             16.2%; Score 113.5; DB 4; 28.5%; Pred. No. 0.00074; ative 22; Mismatches 55;
 -RKDSGAGNFMAGQKGSFPVKENTSYTF 137
                                                                                                                                                                             Length 167;
                                                                                                                                               Indels 31;
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KALNYTSGE---KKISPGIYNDQVMVGYYVN 136

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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25, Appropriate Publication No.
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PRIOR FILING DATE: 2000-01-10
PRIOR APPLICATION NUMBER: 08/788,145
PRIOR FILING DATE: 1997-01-24
PRIOR APPLICATION NUMBER: 08/243,482
PRIOR FILING DATE: 1994-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wolf, Marcia K.
APPLICANT: Cassels, Frederick J.
APPLICANT: Boedeker, Edgar C.
APPLICANT: Boedeker, Edgar C.
TITLE OF INVENTION: TRANSFORMED BACTERIA PRODUCING CS6 ANTIGENS AS VACCINES FILE REFERENCE: 034047.033.3
CURRENT APPLICATION NUMBER: US/10/754,641
CURRENT FILING DATE: 2004-01-12
PRIOR APPLICATION NUMBER: US/08/981,097
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: PCT/DK97/00336
PRIOR FILING DATE: 1997-08-20
PRIOR APPLICATION NUMBER: 08/701,458
PRIOR FILING DATE: 1996-08-22
                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/267,989
                                                                                                                                                                                                     APPLICANT: MADSEN, SOCRED
TITLE OF INVENTION: METABOLICALLY ENGINEERED LACTIC ACID BACTERIA AND
TITLE OF INVENTION: MEANS FOR PROVIDING
TITLE OF INVENTION: SAME
                                                                                                                                                                                                                                                                                                                                                                                           ENERAL INFORMATION:
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                                                                                                                                                                                       FILE REFERENCE: ARNAU=1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                APPLICANT: ARNAU, JOSE
APPLICANT: VRANG, ASTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 167
TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                  PLICANT:
                                                                                                                                                                                                                                                                                                                          PLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 KALNYTSGE---KKISPGIYNDQVMVGYYVN 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 LTSSGQQIGKLVNVNNPDQNMNYYI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 KSLDVNVNIEONFI-PDIDSAVRIIPVNYDSDPKLDSOLYTVEMTIPAGVSAVKIAPTDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
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Similarity 28.5%; Pred. No. 0.00
43; Conservative 22; Mismatches
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                                                                                                                                                                                                                                                                                              ISRAELSEN, Hans
JOERGENSEN, Flemming
                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10267989
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ches 55;
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GENERAL INFORMATION:

APPLICANT: Cao, Yongwei APPLICANT: Hinkle, Gregory J. APPLICANT: Slater, Steven C. APPLICANT: Goldman, Barry S. APPLICANT: Chen, Xianfeng Sequence 21384, Application US/10369493 Publication No. US20030233675A1

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RESULT 10
US-10-369-493-21384
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                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Clostridium pasteurianum US-10-357-567-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 25
LENGTH: 740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/10357567 Publication No. US20040038382A1
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                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/357,567
CURRENT FILLING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/072,433
PRIOR FILLING DATE: 1998-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Compositions and Methods for Bioremdiation FILE REFERENCE: OHU-07748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/046,845 PRIOR FILING DATE: 1997-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Coschigano,
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                     395 PIYGDDYAIACCVSAMRVGKDMQFFGARCNLAKCLLLAINGGVDEK-
                                                                                                                                                                                                                               336 LVTKNSFRYLHTLINLGSAPEPNMTVLWSENL-PESFKKFCAEMSILTDSIQYENDDIMR 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                448 DIEPITDEVLDY----EKVKENYFKVLEYMAGLYVN 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 N-QQITFKALNYTSGEKKISPGIYND-QVMVGYYVN 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 PIYGDDYAIACCVSAMRVGKDMQFFGARCNLAKCLLLAINGGVDEK---
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                                                                         448 DIEPITDEVLDY----EKVKENYFKVLEYMAĞLYVN 479
                                                                                                                 103 N-QQITFKALNYTSGEKKISPGIYND-QVMVGYYVN 136
                                                                                                                                                                                           59 PVYDEDYGL---
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                                                                                                                                                                                                                                                                 4 IATKN-FPVSTTISKSFFAPEPRIQPSFGENVGKEGALLFSVNLTVPENVSQV----TVY 58
                                                                                                                                                                                                                                                                                                           l Similarity 25.(
39; Conservative
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25.0%; Pred. No. 44
                                                                                                                                                                                                                                                                                                                           11.1%; Score 77.5;
25.0%; Pred. No. 4:
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                                                                                                                                                                                                                                                                                                             22;
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                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                         -GRLVNTADASQSIIYQIVDEKGKKMLKDHGAEVTP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
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JS-10-369-493-21384
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Publication No. US20040029129A1
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TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
15Q ID NO 21384
LENGTH: 557
                     Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URRENT APPLICATION NUMBER: US/10/282,122A
                                                                                                                                           DR APPLICATION NUMBER: 60/230,347
DR APPLICATION NUMBER: 60/230,347
DR APPLICATION NUMBER: 60/242,578
DR FILING DATE: 2000-10-23
DR APPLICATION NUMBER: 60/253,625
DR FILING DATE: 2000-11-27
DR APPLICATION NUMBER: 60/257,931
DR APPLICATION NUMBER: 60/257,931
DR APPLICATION NUMBER: 60/257,636
DR APPLICATION NUMBER: 60/267,636
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                                                                         APPLICATION NUMBER: 60/
FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/191,078 FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 NLTVPENVSQVTVYPVYDEDYGLGRLVNTADASQSIIYQIVDEKGKKMLKDHGA 98
                                                                                                                              LING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INVENTION: Identification of Essential Genes in Microorganisms
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Yamamoto, Robert
Forsyth, R.
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Trawick, John
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Zyskind, Judith
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Malone, Cheryl
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27.2%; Pred. No.
                                                                                                    60/269,308
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                                                    See File Wrapper or PALM
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; TYPE: PRT; ORGANISM: Proteus mirabilis US-10-282-122A-68607
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                                                   Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67315
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Publication No. US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: US/10/282,122A CURRENT FILING DATE: 2003-02-20
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                 PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NITLE OF INVENTION: Identification of Essential Genes in Microorganisms
ORGANISM: Pasteurella multocida
                                                                                                                                                                                                                               APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/253,625
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                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/230,347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1422 TTAKVKNETIS------NMOPHAGESITYKAYLVDNHDNEVGMGVEVAWSTNEG 1469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
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43; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                           CATION NUMBER: 60/230,335
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Zyskind,
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Pred. No.
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                                                                                                                    See File Wrapper or PALM
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// ORGANISM: Acinetobacter baumannii
US-10-282-122A-44691

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  Matches
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Best Local Similarity
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SOFTWARE: PatentIn version
EQ ID NO 44691
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLE OF INVENTION: Identification of Essential Genes in Microorganisms ILE REFERENCE: ELITRA.034A URRENT APPLICATION NUMBER: US/10/282,122A URRENT FILING DATE: 2003-02-20
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                  Local
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                                                                                                                                                                                                                              APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
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APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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Malone, Cheryl
Haselbeck, Robert
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Forsyth, R.
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Trawick, John
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Zyskind, Judith
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21.4%; Pred. No. 16;
tive 25; Mismatches
10.7%; Score 75; DB 26.0%; Pred. No. 67; tive 19; Mismatches
                                      DB 4; Length 640;
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  47; Indels
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US-09-815-242-11293
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                                                                   US-10-282-122A-58624
                                                                                           RESULT 15
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US-09-815-242-11293
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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LENGTH: 736
                   Sequence 58624, Application US/10282122A
Publication No. US20040029129A1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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INFORMATION:
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Zyskind, Judith W
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                                                                                                                                                                                                                                                                                                                                               10.7%; Score 75; DB
19.7%; Pred. No. 82;
ative 29; Mismatches
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APPLICANT: Wang, Liangsu APPLICANT: Zamudio, Carlo APPLICANT: Malone, Cheryl

Carlos

Haselbeck, Robert Ohlsen, Kari Zyskind, Judith

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APPLICANT: wall, Daniel
APPLICANT: Travick, John
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APPLICANT: Vamamoto, Robert
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GenCore version 5.1.7
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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// SIDSS/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

// SIDSS/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

// SIDSS/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

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Match Length DB
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                                             US-11-195-739-6
US-11-096-568A-32646
US-11-096-568A-32646
US-10-793-626-2774
US-11-194-285-282
US-11-194-286-282
US-11-194-286-282
US-11-194-367A-333
US-11-196-568A-6311
US-11-096-568A-6311
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US-11-096-568A-6310
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32646, Appli
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US-10-821-234-1182	US-11-051-724-42	US-10-506-454-501	US-10-517-939-164	US-10-995-561-913	US-10-995-561-910	US-11-051-720-1447	US-11-051-720-1446	US-10-995-561-915	US-10-995-561-912	US-10-995-561-914	US-10-995-561-911	US-11-051-720-1372	US-11-051-720-1374	US-11-051-720-1373	US-11-051-720-1375	US-10-467-657-7922	US-11-087-099-8619	US-11-087-099-5784	10 11 400 4000 1100
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1182, A	42, Appl	•	164, App	913, Ap	•	1447, A	1446, A		912, App			1372, A	1374, A	1373, A	1375, A	7922, A	8619, A	5784, A	

ALIGNMENTS

GENERAL INFORMATION: APPLICANT: ALZARI, PEDRO APPLICANT: BOITEL, BIRGITTE APPLICANT: VILLARINO, ANDREA APPLICANT: VILLARINO, ANDREA APPLICANT: VILLARINO, ANDREA APPLICANT: COLE, STEWART TITLE OF INVENTION: PAGH KINASE AND PSTP PHOSPHATASE AND METHODS OF IDENTIFYING TITLE OF INVENTION: INHIBITORY SUBSTANCES FILE REFERENCE: 252853US CURRENT APPLICATION NUMBER: US/11/195,739 CURRENT FILING DATE: 2005-08-03 PRIOR APPLICATION NUMBER: US/10/892,170 PRIOR APPLICATION NUMBER: US/0487,943 PRIOR APPLICATION NUMBER: US 60/487,943 PRIOR PILING DATE: 2003-07-18 NUMBER OF SEQ ID NOS: 20 COMMANDE OF SEQ ID NOS: 20 Ś 밁 δ 밁 밁 Ś ; LENGTH: 268 ; TYPE: PRT ; ORGANISM: Thermobifida fusca US-11-195-739-6 SOFTWARE: | Sequence 6, Application US/11195739 Publication No. US20060019324A1 Matches Query Match Best Local Similarity 161 -EVTVVBEHHDEVPEGHVISQEPBAETTVGAGQSVTLTVSSGPELVEVPDIRGWKVDKAR 220 112 TVITTKPAPGEKANREESVTLTISAGF--PMPNV---VGQKVDDARRLLESSDL----- 160 19 53 2 TEIATKNFP------VSTTISKSFFAPEPRIQPSFGENVGKEGALLFSVNLTVPENV 52 PatentIn version 3.2 KMIKDHGAEVTPNQQITFKALNYT-SGE 117 SQVTVYPVYDEDYGLGRLVN-----TADASQSI-----IYQIVD-----EKGK 90 KELEERGFEVTVHQVIGNRVGDYNPKGE 247 11.2%; ilarity 26.4%; Conservative 2 ; Score 78; DB 7; ; Pred. No. 1.4; 22; Mismatches 4 43; Length 268 Indels 44; 219

RESULT 2 US-11-096-568A-32647 ; Sequence 32647, Application US/11096568A ; Publication No. US20060048240A1

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RESULT 4
US-10-793-626-2774
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; OTHER INFORMATION: Ceres Seq. ID no. 13593732
US-11-096-568A-32647
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; LOCATION: (1)..(361)
; OTHER INFORMATION: Ceres Seq. ID no. 13593731
US-11-096-568A-32646

                                    Sequence 2774, Application US/10793626 Publication No. US20050255478A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 32646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 32647
LENGTH: 356
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Best Local
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APPLICANT: KIMMERLY, WILLIAM JOHN TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS. AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Alexandrov, Nickolai et al
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jblication No. US20060048240A1
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IITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEATURE: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
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                                                                                                                                                                              76 ----NFKTLNEAIKSIPTGNKNRVIIKLAPGVYNEKVTI 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 IPENRAOIPQWFKTNVKPYSQRKGTLDPALEAAEAARQII--TVNQKG----
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                                                                                                                                                                                                                                                       28 IPENRAQIPQWFKTNVKPYSQRKGTLDPALEAAEAARQII--TVNQKG---
                                                                                                                                                                                                                                                                                              48 VPENVSQV-----TVYPVYDEDYGLGRLVNTADASQSIIYQIVDEKGKKMLKDHGAEVT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361
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Pred. No. 3.9;
L6; Mismatches
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Pred. No. 3
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PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2774
LENGTH: 400
                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
SEQ ID NO 166
LENGTH: 375
TYPE: PRT
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: P100629WO CURRENT APPLICATION NUMBER: US/10/485,517 CURRENT FILING DATE: 2004-02-02
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: GB 0118825.9 PRIOR FILING DATE: 2001-08-02 PRIOR APPLICATION NUMBER: GB 0200349.9 PRIOR FILING DATE: 2002-01-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: University of Sheffield APPLICANT: Biosynexus Incorporated
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equence 166, And indication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
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                                 107 TFKALNYTSGEKKISPGIYNDOVM----VGYYVN 136
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87
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                                                                                                    61 YDEDYGLGRLVNT-----
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 NSEVLEYDEVFKKF--
                                                                    YGDDYGIACCVSAMTIGKOMOFFGARANLAKTLLYAINGGKDEK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foster, Simon
Mond, James
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o. US20050256299A1
                                                                                                                                    Conservative
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                                                                                                                                                    10.4%;
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                                                                                                                                    Score 72.5; DE
Pred. No. 8.4;
15; Mismatches
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Pred. No. 5
   -DOMMDWLAGVYIN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                    -ADASQSIIYQIVDEKGKKMLKDHGAEVTPN-QQI 106
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                                                                                                                                        Indels
                                                                        SGAQVGPNFEGI
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RESULT 6 US-10-517-939-362

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; LOCATION: (1)...(26)
JS-10-517-939-362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 282, A Publication No.
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 362
                                                                                         SOFTWARE: PatentIn version 3.0 
EQ ID NO 282
                                                                                                                                                        FILE REFERENCE: 00592.US1 (M&R 268.05920101)
CURRENT APPLICATION NUMBER: US/11/194,246
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2001-10-19
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PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
                                                                                                                                       TUMBER OF SEQ ID NOS: 621
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                                                                                                                                                                                                                                                                                                                      PPLICANT: Mott, John

PPLICANT: Tregod, Catherine

PPLICANT: Treddeon, Staffan

ITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET

ITLE OF INVENTION: USE

ITLE OF INVENTION: USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1680
TYPE: PRT
ORGANISM: Unknown
ORGANISM: HAEMOPHILUS INFLUENZAE
1-194-246-282
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OTHER INFORMATION: Obtained from an environmental sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LE REFERENCE: 564462007901
RRENT APPLICATION NUMBER: US/10/517,939
RRENT FILING DATE: 2004-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM TLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLICANT: Steer, Brian
                                                                 ENGTH: 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1032 RTNVAPAATTWTIDVTLS-----RLQINTLLNAGQRGLRIQTGNAPTVTITIDDVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1144 TAENGHKPSSIAGPENSFTVPEPEQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 YPVYDED-------YGLGR------LVNTADASQSIIYQ---I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YQIGDIDTAGLPLPPQWNFDLPRLSELFEPYFGLGNIYSTETLMNANETKRAFLHHFNVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDEKGKKMLKDHGAEVT-----PNQQITFKALNYTSGEKKISPGIYNDQVMVGY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Esteghlalian, Alireza
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Healey, Shaun
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o. US20050272089A1
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5. US20060003433A1
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Pred. No. 84;
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US-11-124-367A-330

Publication No. US200600247
GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: Hongjin Huang

Sequence 330, Application US/11124367A Publication No. US20060024700A1

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SEQ ID NO 7
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Best Local
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                                                                                                                                                   Best Local
                                                                                                                                                                 Query Match
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PRIOR FILING DATE: 2002-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/098,010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1998-05-13
                                                                                                                                                                                                               NAME/KEY: misc-feature
OTHER INFORMATION: Incyte Clone 2948818
                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITLE OF INVENTION: CELL SIC
LE REFERENCE: PF-0521 PCT
                                                                                                                                                                                                                                                                                                      ENGTH: 898
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                                                                   351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 MGINAVKGVEIGDGFAVVEORG----SEHRDEMTPN---GFES-NHAGG---
   402 FIRDEAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/11/099,691 FILING DATE: 2005-04-06
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                                                                                               28 PSFGENVGKEGALLFSVNLTVPENVSQVTVYPVYDEDYGLGRLVNTADASQSIIYQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 NTADASQSII----YQIYDEKÇKKMIKDHGAEVTPNQQITFKALNYTSGEKKISPGIYND 127
                                  84 - IVDEKGKKMLKDHG---AEVTPNQQITFKALNYTSGEK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 25.8
32; Conservative
                                                                                                                                                   Similarity
                                                                   PSMSVSTGSQSSSVNSMQEVMDESSSELVM--MHDDE-----STINSSSSVVHKKDHV 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAUGHN, Mariah R. YANG, Junming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YUE, Henry
TANG, Y. Tom
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HILLMAN, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATTERSON, Chandra
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                        ID NOS: 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2005-04-06
                                                                                                                                                   10.1%; Score 70.5;
23.2%; Pred. No. 45;
-HGDPRPEPRPTQSVQSQALHYRNRER 434
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CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEO ID NOS: 34460
                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-11-124-367A-333
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                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 333
LENGTH: 898
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: CL001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
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                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 34460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/568,846 PRIOR FILING DATE: 2004-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPLICANT: Michele Cargill
APPLICANT: Hongjin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 898
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LE REFERENCE: CL001519.ORD
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Local Similarity 23.2%; Pred. No. 45;
hee 23; Conservative 26; Mismatches
                                                                                                                                                                                             Local
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                                                                                 351 PSMSVSTGSQSSSVNSMQEVMDESSSELVM--MHDDE---
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                                       84 - IVDEKGKKMLKDHG---AEVTPNQQITFKALNYTSGEK 118
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23; Conservative
FIRDEAG-----HGDPRPEPRPTQSVQSQALHYRNRER 434
                                                                                                                                PSFGENVGKEGALLFSVNLTVPENVSQVTVYPVYDEDYGLGRLVNTADASQSIIYQ----
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                                                                                                                                                                        10.1%; Score 70.5; [
23.2%; Pred. No. 45;
tive 26; Mismatches
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RESULT 11 US-11-096-568A-6312

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; LOCATION: (1)..(379)
; OTHER INFORMATION: Ceres Seq. ID no. 14314720
US-11-096-568A-6312
                                        RESULT 13
US-11-096-568A-6310
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Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 6311
TENCETH. A16
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Sequence 6310, Application US/11096568A Publication No. US20060048240A1
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SEQ ID NO 6312
LENGTH: 379
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CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Therby
                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(416)
OTHER INFORMATION: Ceres Seq. ID no. 14314719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 416
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290 GKEDFIVYGVNLTF-VNLEBANIYDGWNLNGQKFIMANCTFRGVSDKGVVLVLPAPEDDE. 348
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l Similarity 25.6%;
22; Conservative
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1 Similarity 25.6%; Pred. No. 17;
22; Conservative 11 "."
                                                                                                                          DGGNGRIV-TVSLPREELYQLKDKLG 410
                                                                                                                                                                                                     GKEDFIVYGVNLTF-VNLEEANIYDGMNLNGQKPIMANCTFRGVSDKGVVLVLPAPEDDE 385
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                                                                                                                                                                                                                                                                                                        Score 69.5;
Pred. No. 20;
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APPLICANT: Alexandrov, Nickolai et al

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CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 6310
LENGTH: 450
TYPE: PRT
ORGANISM: Glycine max
PEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(450)
OTHER INFORMATION: Ceres Seq. ID no. 14314718
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US-11-087-099-3301
; Sequence 3301, Application US/11087099
; Publication No. US20060041961A1
; Publication No. US20060041961A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Staphylococcus aureus subsp. aureus MW2
JS-11-087-099-3301
                                                                                   Sequence 2208, Application US/10793626 Publication No. US20050255478A1 GENERAL INFORMATION:
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SEQ ID NO 3301
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Best Local Similarity 25.6%;
Matches 22; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.9%; Score 69; DB 7; Length 501
Best Local Similarity 25.6%; Pred. No. 29;
Matches 33; Conservative 17; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
                  APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
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LE OF INVENTION: Therby
E REFERENCE: 2750-1592PUS2
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                                                                                                                                                                                                                                                                                                                                                                                                                         262 ENFKAMDYIIQGGSQPLPSIQAAFKQYGINIINGYGLTEAPLVLVN--TPENSKR-----
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                                                                                                                                                                                                                                                                                                                                                                             60 VYDEDYGLGRLVNTADASQSIIYQIVDEKGKKMLKDHGAEVTPNQ--QITFKALNYTSGE 117
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                                                                                                                                                                                                                                             KNVTPGYWN 359
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Pred. No. 22;
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PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2208
LENGTH: 278
                                                                                                                                                                      Query Match 9.8%;
Best Local Similarity 30.4%;
                                                                                                                                                    Matches
                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                           FEATURE:
114 FVYAWRKVVNPKTASE-FAYIMSDIKNADEVNAGKKSVKDLG 154
                                                                                                                                                    31; Conservative
                                      63 EDYGLGRLVNTADASQSIIYQIVDEK-----
                                                                          57 DIAAQAFEGLYTLNKEDKA-EPAIAKSFPKK--SNGGKTLTINLKKNAKWSNGDSVTAYD 113
                                                                                                              3 EIATKNFPVSTTISKSFFAPEPRIOPSFGENVGKEGALLFSVNLTVPENVSOVTVYPVYD 62
                                                                                                                                                      12; Mismatches
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Pred. No. 15;
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                                      GKKMLKDHG
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Search completed: April 10, 2006, 10:25:42 Job time : 25 secs

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Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abse/ARSSWEB apoolV1210768093/runat_10042006_090301_4503/app_query.fasta_1
-Q=/abse/ARSSWEB apoolV1210768093/runat_10042006_090301_4503/app_query.fasta_1
-Q=-abse/ARSSWEB apoolV1210768093/runat_10042006_090301_4503/app_query.fasta_1
-DB=A Geneseq -QFMT=fastan -SUFFIX=n2.rag mINWATCH+0.1 -LOOPCL=0 -LOOPEXT=0
-DB=A Geneseq -QFMT=fastan -SUFFIX=n2.rag mINWATCH+0.1 -LIST=45
-DCCALIGN=200.*THR_SCORE=pct -THR_MAX=100 -THR_NIN=0 -ALIGN=15 *MODE=LOCAL
-DCCALIGN=200.*THR_SCORE=pct -THR_MAX=100 *THR_NIN=0 +ALIGN=15 *MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs802p
-USER-US10768093_@CGN 1_1_346_@runat_10042006_090301_4503_.NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 *MAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-NARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                   4006
                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                              Score
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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• .	Boedeker EC;		7.	3		•		; origin of replicati CS6A; CS6B; enterotox	gen cssA protein.			154 AA.	ALIGNMENTS	ABR41064 ADD18976	7331	193	825	7	546	72	ADY18325 ABP69277	229	000	927	999	531	550	767	9 6 3	983	211	541	4920	6843 9511	4106
		-				•		<pre>coxigenic E. coli;</pre>						Abr41064 Human MAP Add18976 Human dis	3319 Human	1938 Prost	3296 Human	0779 Ara	5463 A.)781 Ara	3325	626 Hur	1063 Hur)278 Hur	661 Nov	5319 St	3582 Ent	7679 L.)635 All	9836 Ba)460 L.	415 As	208 V.chol	115 E. f	.065 Human MA

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RESULT 2
ADW47733
ID ADW4
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DE E. C
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Query Match:
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Best Local Similarity:
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                                      21-APR-2005
                                                                      ADW47733,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
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                                                                                                     ADW47733 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluProArgIleGlnProSerPheGlyGluAsnValGlyLysGluGlyAlaLeuLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTGTGAACTTAACTGTTCCTGAAAATGTATCCCAGGTAACGGTCTACCCTGTTTATGAT 302
                                                                                                                                                                                                                                                          GlnIleValAspGluLysGlyLysLysMetLeuLysAspHisGlyAlaGluValThrPro
                                                                                                                                                                                                                                                                                                                               CAGATTGTTGAGAAAGGGAAAAAAATGTTAAAAGATCATGGTGCAGAGGTTACACCT
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Best Local Similarity:
                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                       The invention relates to a method of inducing in a susceptible host, the production of antibodies against CS6 protein comprising giving a composition of matter made of bacteria transformed with a plasmid, which contain genes cssA and cssB, all of cssC and DNA sequence cssD that encodes at least 802 amino acids (at least 2406 base pairs), an origin of replication, a Lac promoter, and a kanamycin resistance gene, where the bacteria overexpress both CS6A and CS6B proteins. The method and proteins are useful for stimulating protective antibodies against enterotoxigenic Bscherichia coli. This sequence corresponds to the E. coli CS6 ccsA
                                                                                                                                                                                                                                                                                                                                                                                                                                             Inducing in a susceptible host, the production of antibodies against CS6 protein, useful for stimulating protective antibodies against Escherichia coli by administering a composition comprising bacteria transformed with a plasmid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAY-1994; 94US-00243482
24-JAN-1997; 97US-00788145
10-JAN-2000; 2000US-00479877
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(CASS/) CASSELS F J.
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AGTGTGAACTTAACTGTTCCTGAAAATGTATCCCAGGTAACGGTCTACCCTGTTTATGAT
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                                                   The invention relates to a method of inducing, in a susceptible host, the production of antibodies against a CS6 protein, comprising administering a composition of matter comprising bacteria transformed with a plasmid containing genes cssA, cssB, cssC and cssD; an origin of replication, a Lac promoter and a kanamycin resistance gene, where the bacteria expresses both CS6A and CS6B proteins. The invention also relates to a composition of matter comprising a protein in a pharmaceutical carrier is a carbonated liquid. The method is useful for inducing the production of antibodies against the CS6 protein. The protein and composition are used as vaccines for preventing pathological effects of enterotoxigenic E. coil. This sequence represents a CS6 related protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inducing the production of antibodies against CS6 protein, useful preventing pathological effects of enterotoxigenic E. coli, by administering a composition comprising transformed bacteria produc
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24-JAN-1997; 97US-00788145.
10-JAN-2000; 2000US-00479877
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Alignment Scores:

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coli by administering
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24-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibacterial; vaccine; DNA purification; colonization factor
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                  Inducing in a susceptible host, the production of antibodies against CS6 protein, useful for stimulating protective antibodies against Escherichia coli by administering a composition comprising bacteria transformed with
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) BOEDEKER E C
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  12-AUG-2004
                        US2004156829-A1
                                                                  CS6; cssA; cssB; cssC; cssD; origin of replication; Lac promoter; kanamycin resistance gene; CS6A; CS6B; enterotoxigenic E. coli; Escherichia coli E8775.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inducing the production of antibodies against CS6 protein, preventing pathological effects of enterotoxigenic E. coli, administering a composition comprising transformed bacteria
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24-JAN-1997; 97US-00788145
10-JAN-2000; 2000US-00479877
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ArgLysAspSerGlyAlaGlyAsnPheMetAlaGlyGlnLysGlySerPheProValLys 130
                                                                                                      LysileAlaProThrAspSerLeuThrSerSerGlyGlnGlnIleGlyLysLeuValAsn
                             TTAAAAGATCATGGTGCA-----
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                                                       ValAsnAsnProAspGlnAsnMetAsnTyrTyrIle---
                                                                                 ACCGCTGATGCTTCCCAATCAATAATCTACCAGATTGTTGATGAGAAAGGGGAAAAAAATG
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                                                                                                                                          -GTTTATGATGAAGATTATGGGTTAGGACGACTAGTAAAT
                                                                                                                                                                                                                                                                                                               -AAAAACTTCCCAGTATCAACGACTATTTCAAAAAGTTTT 173
                                                                                                                                                                                                                                                                                                                                                                                                    (1-167)
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Best Local
Query Match
DB:
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ADW47734
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                                                     US-10-768-093-4 (1-527) x ADW47734
                                                                                                       Percent Similarity:
Best Local Similarity:
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                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                            The invention relates to a method of inducing in a susceptible host, the production of antibodies against CSG protein comprising giving a composition of matter made of bacteria transformed with a plasmid, which contain genes cssA and cssB, all of cssC and DNA sequence cssD that contain genes that a contain contain genes cssA and cssB, all of cssC and DNA sequence cssD that conceant the contain contain cssA and cssB, all of cssC and DNA sequence cssD that conceant cssA and cssB, all of cssC and DNA sequence cssD that conceant cssA and cssB.
                                                                                                                                                                                                                                                                                                                                                                                                       Inducing in a susceptible host, the production of antibodies against CS6 protein, useful for stimulating protective antibodies against Escherichia coli by administering a composition comprising bacteria transformed with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAY-1994;
24-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E. coli CS6
                                                                                                                                                                                    Sequence 167
                                                                                                                                                                                                                             replication, a Lac promoter, and a kanamycin resistance gene, where the bacteria overexpress both CS6A and CS6B proteins. The method and proteins are useful for stimulating protective antibodies against enterotoxigenic Escherichia coli. This sequence corresponds to the E. coli CS6 ccsB
                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2005-131784/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wolf MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JAN-2004; 2004US-00754641
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LeuLysLysIleIleSerAlaIleAlaLeuIleAla-----GlyThrSerGlyValVal
            ATGAAGAAAAATTGGTTTAATTCTAATTCTTGCTTCATTCGGCAGCCATGCCAGAACA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyTyrSerSerGlyThrTyrAlaGlyAsnLeuThrValSerPheTyrSerAsn
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Conservative:
Mismatches:
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RESULT 7
ADRI4917
ID ADRI4917
AC ADRI1
XX ADRIA
DT 04-N
DT 04-N
DT 056
KW CS6;
KW kana
XX Unid
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XX Unid
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                                                                  Inducing the production of antibodies against CS6 protein, preventing pathological effects of enterotoxigenic E. coli, administering a composition comprising transformed bacteria
                                                                                                                                                                                     13-MAY-1994; 94US-00243482
24-JAN-1997; 97US-00788145
10-JAN-2000; 2000US-00479877
                                                                                                                                        Wolf MK,
                                                                                                                                                                                                                                                                                                                            CS6; cssA; cssB; cssC; cssD; origin of replication; Lac kanamycin resistance gene; CS6A; CS6B; enterotoxigenic I
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                                    Claim
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                                                                                                                                                               US SEC OF ARMY
                                    SEQ
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                                    English
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The invention production of

relates to a method of inducing, antibodies against a CS6 protein,

in a susceptible host, the comprising administering

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AAE37981

ID AAE3

XX AAE

AC AAE

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Query Match:
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Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer; psoriasis; thromobocytopaenia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease; neurological disorder; Parkinson's disease; epileps; glomerulonephritis; autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome; acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; acquired immune deficiency syndrome; immunosuppressive; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a composition of matter comprising bacteria transformed with a plasmid containing genes casA, casB, casC and casD, an origin of replication, a Lac promoter and a kanamycin resistance gene, where the bacteria expresses both CSGA and CSGB proteins. The invention also relates to a composition of matter comprising a protein in a pharmaceutical carrier. The pharmaceutical carrier is a carbonated liquid. The method is useful for inducing the production of antibodies against the CSG protein. The protein and composition are used as vaccines for preventing pathological effects of enterotoxigenic E. coli. This sequence represents a CSG
                                                                                                                                                                                                                                                                                                                                                         Human kinase
                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACGATCAGGTTATGGTTACTATGTAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerAlalle---TyrThrGlyGlyGluTyrProAsnSerGlyTyrSerSerGlyThrTyr 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGCGCTGAATTATACTAGCGGGGAA-----AAAAAAATATCTCCTGGAATATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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MetThrGlyTyrGlySerHisSerLysValTyrSerGlnSerLysAsnIleProLeuSer CTTGCTTCATTCGGCAGCCATGCCAGAACAGAAATAGCGACTAAAAACTTCCCAGTATCA

60

---ACGACTATTTCAAAAAGTTTTTTTGCACCTGAACCACGAATACAG---

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Alignment
Pred. No.:
                                                                                                                                                                               US-10-768-093-4 (1-527) x AAE37981
                                                    Query Match:
                                                                       Percent Similarity:
Best Local Similari
                                                                                                                                                                                                                          CC and phosphatase (KPP). KPP agonists and antagonists are useful for CC diagnosing, treating or preventing disorders associated with aberrant CC expression of KPP, particularly cell proliferative disorders (e.g. arteriosclerosts, atherosclerosts, clirhosts, hepatitts, paroxysmal nocturnal haemoglobhnuria, polycythaemia vera, psoriasis, primary CC thromobocytopaenia or cancer), developmental disorders (e.g. renal tubular cardosis, antenia, polycythaemia vera, psoriasis, primary CC thromobocytopaenia or mental retardation), neurological disorders (e.g. Alheimer's disease, Parkinson's disease or epilepsy), autoimmune/ CC inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome, CC disease, diabetes mellitus, glomerulonephritis, contact dermatitis, Crohn's CC disease, diabetes mellitus, glomerulonephritis, fortiable bowel syndrome, CC gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome, CC multiple sclerosis, osteoarthritis, osteoporosis, panoreatitis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral, bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP Ci suseful in assessing the effects of exogenous compounds on the cosperior of nucleic acids and kinases and phosphatases. KPP gene is clieses The meneral as human KPD profesi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-2001;
19-DEC-2001;
21-DEC-2001;
04-FEB-2002;
15-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disc. (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis cancer or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated polypeptide, which and phosphatase (KPP). KPP agonists and antagonists are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-532894/50.
N-PSDB; AAD57353.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 230; 282pp; English
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                                                                       Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AJA,
                                                                                                                                                                               221 AA;
                                                                                                                                                                                                                The present sequence is human KPP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 2001US-0343007P.
; 2001US-0343546P.
; 2002US-0354388P.
; 2002US-0357675P.
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Emerling BM,
                                                    0.0198
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42.2$
25.5$
9.9$
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g BM, Ramkumar J, Jin P,

K, Lehr-Mason PM, Khare R,

Kprague WW, Zebarjadian Y;
 (1-221)
                                                  Conservative:
Mismatches:
Indels:
                                                                                                         Length:
Matches:
                                   Gaps:
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P, Griffin JA,
R, Lee S, Haw
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The present sequence is that of the C-terminal domain of a Ser/Thr protein kinase of Thermobifida fusca. Sequence homology is shown to the C-terminal domain of Ser/Thr protein kinase PknB ADW47924 of Mycobacterium tuberculosis. M. tuberculosis PknB, PknA and protein phosphatase PstP ADW47922, along with other signaling modulators, co-ordinately regulate cell alongation during growth. The invention provides claimed methods for identifying substances that modulate the activity of M. tuberculosis PknB
                                                                                                                                     Identifying substances that modulates pknB protein kinase or pstp2 phosphatase activity, for identifying antibacterial substances, by comparing the activity from cells contacted with the substance to
                                                                                                                                                                                                                                                                                                                                                                                           Protein kinase; antibacterial;
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31-AUG-2001; 2001JP-00263450
21-JAN-2002; 2002JP-00012176
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CATGGTGCAGAGGTTACACCTAATCAACAATAACTTTTAAAGCGCTGAATTATACTAGC
                                                  AsnThrSerSerVal-----GlnIleIleGluGluHis---ProProMetIleGlnAsn
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CC Enterococcus fascium encoding an Enterococcus fascium polypeptide having CC enterococcus fascium encoding an Enterococcus fascium polypeptide having CC one of 10 fully defined sequences given in the (or comprising 40 CC sequential nucleotides chosen from any of the nucleic acids, its CC complement or sequences hybridising to it). Also included are a CC recombinant vector comprising the nucleic acid operably linked to CC transcription regulatory element, a cell comprising the vector and a CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. CC The nucleic acids is useful for diagnosing pathological conditions cresulting from E. fascium bacterial infection (e.g. urinary tract infection, bacteraemit, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and anterocurrent.
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                                                                                                                                                                                               V.cholerae VPI phage conserved gene AldA protein
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                                                                                                                                           Unidentified.
                            10-MAY-1999;
                                                        10-MAY-2000; 2000WO-US012580
                                                                                   16-NOV-2000
                                                                                                                                                                     Bacteriophage;
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                                                                                                                                                                                                                                                                                                                                             IleAlaIleCysGlyGlySerGlyGluLys 300
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                                                                                                                                                                                                                               (first
                            99US-0133373P
                                                                                                                                                                     pathogenicity island; vaccine; allergy
                                                                                                                                                                                                                                                                                   protein; 506
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(UYMA-) UNIV MARYLAND BALTIMORE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated bacteriophage encoded by a pathogenicity island of a pathogenic bacterium, useful for generating bacteriophage-base vaccines or vectors, e.g. to treat allergies.
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                                         TyrTyrTleLysProThrLeuPhe
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                                                                     AAAAAATATCTCCTGGAATATAT 493
                                                                                                                                                    GlnTyrAspLysIleLeuGlyTyrIleGlnIleGlyLysAspGluGlyAlaGluLeuIle
                                                                                                                                                                                  AAAGGGAAAAAATGTTA--------AAAGATCATGGTGCAGAGGTTACA
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Ct the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid canceling a polypeptide whose expression is inhibited by the antisense comprised whose expression is inhibited by the antisense comprised containing the vector; (3) an isolated containing the polypeptide; (6) inhibited by the antisense contained for containing the vector; (6) inhibited by the containing the polypeptide; (6) inhibited by the containing the polypeptide; (6) inhibiting cellular containing the polypeptide; (6) inhibiting cellular containing the polypeptide; (6) inhibiting cellular containing the gene product or that antibioty against a biological pathway contained for proliferation, or that inhibits cellular proliferation; (6) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism containing strains in which the gene compound that inhibits proliferation of containing the strains is present in a culture or collection of containing or (13) identifying the target of a compound that inhibits the containing the extent of a compound that inhibits the containing the extent of containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the containing the cont
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25-OCT-2001;
08-FEB-2002;
Sequence 541 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 77158; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAR-2002;
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2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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Forsyth
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Alignment Scores

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N-PSDB;
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-QO/Abse/ABSSWEE spool/US10768093/runat 10042006 090304 4553/app_query.fasta_1
-QO/Abse/ABSSWEE spool/US10768093/runat 10042006 090304 4553/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOFCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human10.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-QUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10768093 @CGN 1 163 @runat 10042006 090304 4553 -NCPU=6 -ICPU=3
-USER=US10768093 @CGN 1 163 @runat 10042006 090304 4553 -NCPU=6 -ICPU=3
-NORMAP NEG SCORES=0 -WAIT -DSSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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 TTGACACATTACGAATGTTA...
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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n and fur		- 27	probable integral	hypothetical prote	fimbrial assembly	DNA topoisomerase	chaperone protein	kinesin-related pr		pyruvate-formate l	probable acid-CoA	glycolate oxidase	polyprotein Pl - A	probable potassium	conserved hypothet	o ac	m	SAE2 protein - yea	hypothetical prote	homeodomain-intera	beta-1,4-galactosy	xanthine phosphori	hypothetical prote	acet	e flag	c	e gnti	(2-ph	etical	hypothetical prote

ALIGNMENTS

RESULT 1 I60266 Percent Similarity:
Best Local Similarity:
Query Match: S 밁 S 밁 á R;Willshaw, G.A.; Smith, H.R.; McConnell, M.M.; Rowe, B. FEMS Microbiol. Lett. 49, 473-478, 1988
A;Title: Cloning of genes encoding coll-surface (CS) antigens A;Reference number: I60266 CS6 structural subunit A - Escherichia coli C;Species: Escherichia coli C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004 C;Accession: I60266 US-10-768-093-4 (1-527) x I60266 (1-154) Pred. No.: Alignment Scores: A;Cross-references: UNIPROT:P53508; UNIPARC:UPI000012A400; EMBL:U04844; NID:g442375; PID A; Molecule type: DNA A; Residues: 1-154 < RES> A;Status: preliminary; translated A; Accession: 183 123 21 **I60266** GluIleAlaThrLysAsnPheProValSerThrThrIleSerLysSerPhePheAlaPro 2.12e-69 741.00 98.1% 92.9% 78.9% from Conservative:
Mismatches:
Indels:
Gaps: Length: Matches: GB/EMBL/DDBJ 154 143 8 'n enterotoxigenic Escheri 40

41

GlurroGlnIleGlnProSerPheGlyLysAsnValGlyLysGluGlyGlyLeuLeuPhe

K. F. × Quet

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Percent Similarity:
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C;Accession: 183348
C;Accession: 18348, H.R.; McConnell, M.M.; Rowe, FEMS Microbiol. Lett. 49, 473-478, 1988
A;Title: Cloning of genes encoding coli-surface (CS) A;Reference number: 160266
A;Accession: 183348
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A; Residues: 1-167 < RES>
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;Species: Escherichia coli
;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
;Accession: 183348
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    AlaGlyGlnLysGlySerPheSerValLysGluAsnThrSerTyrThrPheSerAlaIle
                                                             AsnProAspGlnAsnMetAsnTyrTyrileArgLysAspSerGlyAlaGlyLysPheMet
                                                                                               GATGCTTCCCAATCAATAATCTACCAGATTGTTGATGAGAAA.-----GGGAAAAAAATG
                                                                                                                              ValProThrAspSerLeuThrSerSerGlyGlnGlnIleGlyLysLeuValAsnValAsn
                                                                                                                                                           TACCCT-----GITTATGATGAAGATTATGGGTTAGGACGACTAGTAAATACCGCT
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                                     TTAAAAGATCATGGTGCA---GAGGTTACACCTAATCAACAAATAACTTTTAAAGCGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
DB:
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A;Introns: 47/1; 408/1; 448/3; 512/1
A;Note: T20K12.280
C;Superfamily: Arabidopsis thaliana hypothetical protein T20K12.280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein T20K12.280 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47930
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A; Residues: 1-718 <DEH>
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LeuThrValSerPheTyrSerAsn 167
                                     GluCysLysGluThrAlaThrAspAlaGlnGlyLysLeuSerPro
                                                                                                 GlnAlaHisSerProAlaSerProLeuGluSerProThrThrCysSerValArgLeuThr 473
                                                                                                                                 GGTGCAGAG---
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                                                                                                                                                               GTCTACCCTGTTTATGATGAAGATTATGGGTTAGGACGACTAGTAAATACCGCTGATGCT 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RiKaraolis, D.K.R.; Johnson, J.A.; Bailey, C.C.; Boedeker, E.C.; Kaper, J.B.; Reeves, Proc. Natl. Acad. Sci. U.S.A. 95, 3134-3139, 1998
A;Title: A Vibrio cholerae pathogenicity island associated with epidemic and pandemic A;Reference number: Z16672; MUID:98169509; PMID:9501228
A;Accession: T09437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable aldehyde dehydrogenase (NAD) (EC 1.2.1.3) aldA [similarity] - Vibr C;Specias: Vibrio cholerae C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: T09437
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Best Local Similarity:
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A; Residues: 1-506 < KAR>
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Experimental source: strain N16961
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 TyrTyrileLysproThrLeuPhe
                                                                                                                                          GlnTyrAspLysIleLeuGlyTyrIleGlnIleGlyLysAspGluGlyAlaGluLeuIle
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                                 AAAAAATATCTCCTGGAATATAT
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                                   491
                                                                                                                                                                                                                                                                                                                                                                                                ----TTAACTGTTCCTGAAAATGTATCCCAGGTA 281
                                                                                                                                                                            -----AAAGATCATGGTGCAGAGGTTACA 419
                                                                       -GluAsnTyrLeuSerGlyGly 382
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A; Residues: 1-541 <HEI>
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;Experimental source: serogroup O1; strain N16961; biotype El Tor
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TyrTyrileLysProThrLeuPhe
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                                                                         PheGlyGlyHisProAsnAsnGl
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H.; Dragoi, I.; Sellers,
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enolase - fission yeast (Schizosaccharomyces
C/Species: Schizosaccharomyces pombe
(C/Date: 03-Dec-1999 #sequence revision 03-Dec
                                                            RESULT
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A;Residues: 1-439 <JAC>
A;Cross-references: UNIPROT:P40370; UNIPARC:UPI0000168FC9; GB:U13799; NID:g535441; PIDN:
A;Note: The authors translated the codon GTC for residue 20 as B and GAC for residue 83
C;Comment: This glycolytic enzyme catalyzes the dehydration of 2-phosphoglycerate to pho
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Gene 154, 109-113,
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;Superfamily: enolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTATCAACGACTATTTCAAAAAGTTTT-----
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                                                                                                                                                          ACTAGCGGGGAAAAAAAA 473
                                                                                                                                                                                                 CATGGTGCAGAGGTTACACCTAATCAACAAATAACTTTTAAAGCGCTGAAT-----TAT 455
                                                                                                                                                                                                                                                                                ValThrSerSerGluPheTyr-----ValAsp-----GlyLysTyrAspLeuAspIle
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3, 1995
  ccharomyces pombe
#sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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R, Wood, V.; Rajandream, M.A.; Barrell, B.G.; submitted to the EMBL Data Library, May 1999 A; Reference number: Z21875 A; Accession: T39737 A; Status: preliminary; translated from GB/EMB A; Molecule type: DNA A; Residues: 1-439 < WOOD
R; Weidner, G.; Sawers, G.
J. Bacteriol. 178, 2440-2444, 1996
A; Title: Molecular characterization of the A; Reference number: JC6010; MUID: 96218720; A; Accession: JC6010
                                                                                                                     formate C-acetyltransferase (EC 2.3.1.54) - Clostridium N;Alternate names: Pf1 protein; pyruvate formate-lyase C;Species: Clostridium pasteurianum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Experimental source: strain 972h-;
                                                                                       Date: 10-Sep-1999 #sequence_revision; Accession: JC6010; PC6004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspGluGlyGlyIle-----AlaProAspLeuGlnThrProGlnGluAlaLeuAspLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGTGTTATATGAAGAAAACAATTGGT-----TTAATTCTAATTCTTGCTTCA 101
                                                                                                                                                                                                                                                                  ACTAGCGGGGAAAAAAAA 473
                                                                                                                                                                                                                                                                                                   CATGGTGCAGAGGTTACACCTAATCAACAAATAACTTTTAAAGCGCTGAAT----TAT
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                     genes encoding pyruvate formate-lyase PMID:8636053
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                                          and
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A;Description: catalyzes the reversible conversion of acetyl-CoA and formate in A;Pathway: anaerobic glucose metabolism C;Superfamily: formate C-acetyltransferase 1; glycyl radical homology C;Keywords: acyltransferase; coenzyme A; homodimer; lyase; thiolester bond F;681-740/Domain: glycyl radical homology C;Reywords: acyltransferase; coenzyme A; homodimer; lyase; thiolester bond F;685/Active site: Cys (cysteine thiyl radical intermediate) #status predicted F;405/Active site: Cys (cysteine thiyl radical) #status predicted F;715/Active site: Cys (S-acetylcysteine intermediate) #status predicted
RESULT 9
JC7506 spliced variant CD86 deltaTM isoform
C186 spliced variant CD86 deltaTM isoform
C1Species: Homo sapiens (man)
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A;Residues: 1-740 <WEII>
A;Cross-references: UNIPROT:Q46266; UNIPARC:UPI0000131758; EMBL:X93463; NID:g1072360; PI
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C;Comment: This enzyme must be activated by the ite and causes peptide cleavage.
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                                                                                                                AlaGlyLeuTyrValAsn
                                                                                                                                                          GTTGGTTACTATGTAAAC
                                                                                                                                                                                                                                                   AATTATACTAGCGGGGAAAAAAAAATATCTCCTGGAATATATAACGAT---CAGGTTATG 506
                                                                                                                                                                                                                                                                                                                                                                                                                              ACCGCTGATGCTTCCCAATCAATAATCTACCAGATTGTTGATGAGAAAGGGAAAAAAATG
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                                                                                                                                                                                                                                                                                                                                       TTAAAAGATCATGGTGCAGAGGTTACACCTAAT---CAACAAATAACTTTTAAAGCGCTG 449
                                                                                                                                                                                                                                                                                                                                                                                    LeuAlaLysCysLeuLeuLeuAlaIleAsnGlyGlyValAspGluLys----
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C; Accession: AF1226 R; Glaser, P.; Frangeul, L.;

Dominguez-Bernal, G.;

Duchaud,

Buchrieser, C.; Amend, chaud, E.; Durand, L.;

A.; Baquero, I Dussurget, O.;

F.; Berche, P.; Entian, K.D.; 09-Jul-2004

; Bloecker Fsihi, H.

Listeria monocytogenes (strain

A; Authors: Kreft,

Kuhn, M.; Kunst,

F.; Kurapkat,

Madueno,

E)

Maitournam,

Science 294,

.; Jones, L.M.; Karst, cience 294, 849-852, 2

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RESULT 10
AP1226
AP1276
AP1276
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change
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C;Accession: JC7604
R;Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bc
Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
A;Title: Identification of an alternatively spliced variant
A;Reference number: JC7604; MUID:21092744; PMID:11162656
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A; Residues: 1-275 < MAN
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                                                                                                                                                                                   GlnThrLysLysArgGluLysIleHisIleProGluArgSerAspGluAlaGlnArgVal
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                                                                                                                                                                                                                                                                                       GGACGACTAGTAAATACCGCTGATGCTTCCCAATCAATAATCTACCAGATTGTTGATGAG 377
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ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AF1226
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-183 <GLA>
A;Cross-references: UNIPROT:Q8Y7Q8; UNIPARC:UPI0000055539; GB:NC_003210; PIDN:CAC99292.1
A;Experimental source: strain EGD-e
C;Genetics:
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Best Local Similarity:
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A,Molecule type: DNA
A,Residues: 1-13055 <FUL>
A,Cross-references: UNIPROT:Q09165; UNIPARC:UPI000017CF3A; EMBL:U00054; NID:g485140;
                                                       submitted to the EMBL Data Library, May 1994
A,Description: The sequence of C. elegans cosmid
A,Reference number: Z18540
A,Accession: T16580
                                                                                                                                  hypothetical protein KO7E12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #tex C;Accession: T16580
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                                           A;Status: preliminary; translated
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                                              GB/EMBL/DDBJ
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A;Residues: 1-321 <BUL>
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A;Experimental source: strain Bristol C;Genetics:
A;Gene: CESP:K07E12.1
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                                                                                                                                                                                      A; Map position: FOR1257323-1258288
                                                                                                                                                                                                                                        A; Cross-references: UNIPROT: Q58708;
                                                                                                                                                                                                                                                                                                A;Tille: Complete genome sequence of the methanogenic a; A;Reference number: A64300; MUID:96337999; PMID:8688087 A;Accession: G64463 A;Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein MJ1312 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
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42.28
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8.88
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8726/3; 9803/3; 10937/3; 12234/2; 1229
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odek, A.;
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Percent Similarity:
Beet Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                              hypothetical protein all2333 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF2097
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF2097
A;Sterence : ~~1-1-1
                                                                                                                                                                                                                                         A/Status: pro-----
A/Nolecule type: DNA
A/Residuse: 1-595 <KUR>
A/Cross-references: UNIPROT:Q8YULL; UNIPARC:UPI00000CE3D3;
A/Cross-references: Strain PCC 7120
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 ThrAlaArgTyrProValGlnSerProThrTrpValValValMetGlnAspPheGlyGlu 203
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A; Residues: 1-309 «BLAT»
A; Residues: 1-309 «BLAT»
A; Cross-references: UNIPROT; Q46858; UNIPARC: UPI000013BF0E;
A; Experimental source: strain K-12, substrain MG1655
A; Experimental source: strain K-12, substrain MG1655
C; Superfamily: Escherichia coli hypothetical protein b3013
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A;Title: The complete genome sequence of Escherichia coli
A;Reference number: A64720; MUID:97426617; PMID:9278503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ypothetical protein b3013 - Bscherichia coli (strain K-12);Species: Escherichia coli
;Species: Escherichia coli
;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession:
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     TyrGlnAsnTyrLysSerAspAlaThrAlaProTyrPheGlyGluThrGlyGluArgAla
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Mau, B.; Shao,
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Map position: 3
;Introns: 93/1; 468/3; 527/3; 565/3; 600/3; 645/3; 664/2; 696/3; 735/3; 778/1; 821/3
;Note: T12K4.110
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Molecule type: DNA
Residues: 1-951 <MON>
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/Species: Arabidopsis thaliana (mouse-ear cress)
/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT:Q9M298; UNIPARC:UPI000009FF20; EMBL:AL138640 Experimental source: cultivar Columbia; BAC clone T12K4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Rudd, S.; Lemcke, K.; May
bmitted to the Protein Sequence Database, April 2000
Reference number: Z24460
Accession: T47324
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                                                                                                                                                                                207 GlyArgThrLeuAlaValProGlyLeuArgAsnAspValValMetTyrAspArgPheThr 226
                                                                                                                                                                                                                                                                          187 ValAlaProAspThrGlyPheAsnThrSerIleValAsnIleProArgTrpSerProAsp 206
                                                                                                                                                                                                                                                                                                                                                                    167 ThrGlyThrValLeuCysTrpGluLeuGlnAsnGlyValValSerPheThrLeuLysGly 186
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                                                                                         GlyGluLysLeuPheAlaLeu----
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LeuThrTrpAlaProAsn 249
                                      CTGGCATGGCTGCGAAT 101
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Search completed: April 10, 2006, 10:07:31 Job time : 46 secs

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-Q=/abss/ABSSWEB_spool/US10768093/runat_10042006_090303_4519/app_query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bite -START=1 -END=-1 -MTRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DGCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT=pto -NORM=Ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10768093_@CGN 11 466_@runat 10042006_090303_4519 -NCPU=6 -LCPU=3
-NO_MMAP -NEG_SCORES=0 -THAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPFOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Match
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Maximum Match 100%
Listing first 45 summaries
 TTGACACATTACGAATGTTA.....TTGGTTACTATGTAAACTAA 527
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Copyright (c) 1993 - 2006 Biocceleration
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Q5405B_DICDI
Q5405B_DICDI
Q54X50_LEGGPH
Q4X118_STRPN
Q4X118_STRPN
Q4X118_BLDICDI
Q54ED6_DICDI
Q72P37_LEPIN
Q54ED7_LEPIN
Q54ED7_LICDI
Q54ED7_LICDI
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Q9M2C6_ARATH
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WITCHWEINE

Escherichia coli. Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-WAY-2005 (Rel. 47, Last annotation update)
10-WAY-2005 (Rel. 47, Last annotation update)

NUCLEOTIDE SEQUENCE. STRAIN=E8775;

NCBI_TaxID=562;

RESULT 1 F6A2_ECOLI

P53509; 01-OCT-1996 ECOLI

STANDARD;

154 ያ

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Percent Similarity:
                            Alignment Scores: Pred. No.:
                                                                   CHAIN
SEQUENCE
                                                                                              Fimbria;
SIGNAL
                                                                                                                                                                                                                                 Wolf M.K., de Haan L.A.M., Cassels F.C., Willshaw G.A., Gestel E.C.M.
Gaastra W., Warren R., Boedeker E.C.;
Submitted (JAN-1994) to the ENBL/GenBank/DDBJ databases.
-:- FUNCTION: Fimbriae (also called pili), polar filaments radiating
from the surface of the bacterium to a length of 0.5-1.5
micrometers and numbering 100-300 per cell, enable bacteria to
colonize the epithelium of specific host organs.
                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                         EMBL; U04846; AAB51361.1; -;
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                                                                                                         Signal.
                                                                     154 AA;
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154
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CS6 fimbrial subunit A.
CS6 fimbrial subunit A.
; 421E223D9FA5FCB8 CRC64;
 Length:
Matches:
Conservative:
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/ Match:
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01-OCT-1996 (Rel. 34, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation updat
CS6 fimbrial subunit A precursor (CS6 pilin
                          EMBL; U04844; AAC45093.1;
PIR; 160266; 160266.
Fimbria; Signal.
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Enterobacteriaceae; Escherichia.
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                                                                                                     Swiss-Prot entry is copyright. It is produced through a collaboration sent the Swiss Institute of Bioinformatics and the EMBL outstation EDUTOPEAN 1016 to Institute. There are no restrictions on its long as its content is in no way modified and this statement is no
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Willshaw G.A., van Wolf M.K., de Haan L., Cassels F.C., Willshaw G.A., van Gaastra W., Warren R., Boedeker E.C.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
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  This.Swiss-Prot entry is copyright. It is produced through a obstween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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                                                                                                                                                                                                                                  Hypothetical protein. ORFNames=DDB0215209;
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J.A., Gloeckner G., Rajandream M.-A.,
S., Song J., Olsen R., Szafranski K., Xu Q.,
S., Madera M., Konfortov B.A., Rivero F.,
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RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Muzny D., Mones K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Hauser H., Junnes R., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Louiseged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
RA J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Sugano S., White B., Walker D., Woodward J., Kobsenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
"The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0.0-0/2005).

CC Christian C. Caution whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TremBlrel. 28, 25-OCT-2004)
    Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Legionella.
NCBI_TaxID=272624;
[1]
                                                                                                                                                                 OrderedLocusNames=lpg0661;
Legionella pneumophila sub
ATCC 33152)
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05ZXSO; LEGPH PRELIMINARY
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EMBL, AAFT01000071; EAL66967.1; -; Genomic_DNA
Hypothetical protein.
SEQUENCE 440 AA; 50234 MW; FC85D88231E1A694
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Percent Similarity:
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Q4K1L8
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Pred. No.:
Score:
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PubMed=15448271; DOI=10.1126/science.1099776;

Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,

Asamani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,

Steshenko V., Park S.H., Zhao B., Teplitskaya E., Edwards J.R.,

Steshenko V., Park S.H., Zhao B., Teplitskaya E., Edwards J.R.,

Pampou S., Georghiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,

Fampou S., Georghio A., Chou I.-C., Iannuccilli W., Ulz M.E.,

Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.

Segal G., Qu X., Rzhetsky A., Zhang P., Cayanis E., De Jong P.J.,

Ju J., Kalachikov S., Shuman H.A., Russo JJ.;

Ju J., Kalachikov S., Shuman H.A., Russo JJ.;
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GG; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0042626; F:ATPase activity,
GO; GO:004810; P:transport; IEA.
InterPro; IPR000412; ABC_2.
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Pfam; PF01061; ABC2 membrane; 1.
PROSITE; PS51012; ABC_TM2; 1.
                Streptococcus pneumoniae.
Bacteria; Firmicutes; Lac
                                           Putative glycosyl transferase.
Name=wchM; ORFNames=SPC15B_0013, SPC15C_0013,
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Science 305:1966-1968(2004).
                                                                            13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence up
13-SEP-2005 (TrEMBLrel. 31, Last annotation
                                                                                                                          Q4K1L8 STRPN PRELIMINARY;
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EMBL; CR931666; CAI33391.1; -; Genomic_DNA.

EMBL; CR931664; CAI33368.1; -; Genomic_DNA.
                                                                LT 8
Q5 STRPN
Q5 STRPN
Q1 (105 STRPN PRELIMINARY; PRT; 318 AA.
Q4 (105 )
13 - SEP - 2005 (TrEMBLrel. 31, Created)
13 - SEP - 2005 (TrEMBLrel. 31, Last sequence update)
13 - SEP - 2005 (TrEMBLrel. 31, Last annotation update)
Putative glycosyl transferase.
QRFNames=SPC15A_0013;
QRFNames=SPC15A_0013;
        Streptococcus.
NCBI_TaxID=1313;
                                         Streptococcus pneumoniae.
Bacteria; Firmicutes; Lactobacillales;
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STRAIN=553/62, 688/6,
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01-JAN-1998
01-OCT-2003
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NUCLECTIDE SEQUENCE.

MEDLINE=98062131; PubMed=9400959;

Sriskantha A., Osborne R.J., Dall D.J.;

Sriskantha A., Osborn
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037318 HAEPV PRELIMINARY;
037318;
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Viruses; dsDNA viruses, no RNA stage; Pox
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Last annotation updat
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13-SEP-2005 (TrEMBLrel. 3
Hypothetical protein.
ORFNames=DDB0219680;
STRAIN-AX4;

STRAIN-AX4;

SIGNAIN-AX4;

SICHINGER L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,

Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,

Sucgang R., Berriman M., Song J., Olsen R., Strero F.,

Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,

Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,

Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,

Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,

Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
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Submitted (AUG-1997) to the EMBL/GenBank/DDBJ
EMBL; AF019224; AAB96623.1; -; Genomic_DNA.
InterPro; IPR000893; Spheroidin.
Pfam; PF05541; Spheroidin; 1.
SEQUENCE 1007 AA; 115438 MW; 3352847F565B6
                                                                                                                                                                                     Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida;
NCBI_TaxID=44689;
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Q54ED6;
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RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Louiseged H., Mungall K., Oliver K., Price C., Quail M.A.,
Louiseged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
RA J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Kay G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
"The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0/2005).

CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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EMBL; AAFI01000257; EAL61826.1; -; Genomic_DNA
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ValAspTyrGlyIleAsp
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LeuLeuLysAspAsnValGluLeuThrValAspGlnLeuIleThrPheLysIleSer 2473
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Last sequence update)

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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RC STRAIN=Fiocruz LI-130;

RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;

RA Nascimento A.L. T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,

RA Nascimento A.L. T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,

RA HO P.L., Haake D.A., Verjovski-Almedda S., Hartskeerl R.A.,

RA Coutinho L.L., Degrave W.M., Dellagostin O.A., El-Dorry H.,

RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Giglioti E.A.,

RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Hartakava R.,

RA Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,

RA Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,

RA Golveira R.C., Pereira G.G., Reis M.S., Schriefer A.,

Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,

RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;

"Comparative genomice of two Leptospira interrogans serovars reveals

RT novel insights into physiology and pathogenesis.";

DR Bocteriol. 186:2164-2172(2004).

DR MBL; AE017297; AAS71206.1; -; Genomic DNA.

DR GO; GO:00031824; F:catalytic activity; IEA.

GO; GO:00031824; F:catalytic activity; IEA.

GO; GO:00031824; F:catalytic activity; IEA.

GO; GO:00031824; F:catalytic activity; IEA.

GO; GO:0003182; P:penicillin binding; IEA.

GO; GO:0003182; P:penicillin binding; IEA.

GO; GO:0001264; Glyco_trans_51.

DR Ffam; PF00905; Transeply: 1.

Pfam; PF00905; Transeply: 1.

Pfam; PF00905; Transeply: 1.

RA Carboxypeptidase; Complete proceome.

SEQUENCE 918 AA; 102807 MW; 2D9E5321BC396960 CRC64;
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Bacteria; Spirochaetes;
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                                               GCAGAGGTTACACCTAATCAACAATAACTTTTAAAGCG-----CTGAATTATACT
                                                                                                             LeuGlnValAlaLeuValAlaValAspProSerThrGlyGluIleLeuLeuMetHisGly
                                                                                                                                                                                                                       SerProAlaLeuGluLeuPheIleAspThrAspSerPheGlyGlyGlnAsnGluSerGly .556
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GO; GO:0009274; C:cell wall (sensu Bacteria); IE
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0008658; F:penicillin binding; IEA.
GO; GO:000852; F:peptidoglycan biosynthesis; IE
InterPro; IPR001264; Glyco_trans 51.
InterPro; IPR001264; Glyco_trans 51.
InterPro; IPR001460; Pencl_bind_tpept.
Pfam; PF00912; Transgly; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Glyco_trans_51; 1.
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MEDLINB=22598143; PubMed=12712204; DOI=10.1038/nature01597;

Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,

Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-H., Yin H.-F.,

Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,

Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,

Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,

Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,

Xu J.-G., Zhao G.-P.;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Penicillin-binding protein 1A (EC 3.4.-.-) (EC 2.4.2.-)
OrderedLocusNames=LA1009;
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SEQUENCE 918 AA,
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SerProAlaLeuGluLeuPheIleAspThrAspSerPheGlyGlyGlnAsnGluSerGly 556
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                                                                                                             LeuThrAspAsnLysAsnSerSerGluThrAlaValPheArgArgTyrIleGlnAspLeu
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13-SEP-2005 (TrEMBLrel. 31, Last annotation updat
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GO; GO:0004194; F;pepsin A activity; IEA.
GO; GO:0006508; P;proteolysis and peptidolysis;
InterPro; IPR001461; Peptidase_A1.
InterPro; IPR001969; Pept_Asp_AS.
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ EMBL, AL844507; CAD51290.1; -; Genomic_DNA.
HSSP, P00797; 2REN.
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Eukaryota; Alveolata;
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PRINTS; PR00792; PEPSIN.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                         Alignment Scores:
                                                                                                                       EU Arabidopsis sequencing project;
submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL137898; CAB71068.1; -; Genomic_DNA.
PIR; T47930; T47930.
Hypothetical protein.
SEQUENCE 718 AA; 80730 MW; F3DCA7B9379AEB25 CRC64;
                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.

De Haan M., Maarge A.C., Grivell L.A., Mewes P.

Mayer K.F.X., Quetier F., Salanoubat M.;

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat.
Hypothetical protein T20K12.280.
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                                                     GlnAlaHisSerProAlaSerProLeuGluSerProThrThrCysSerValArgLeuThr
                                                                                                        ServalSerArgGluValGluAsnValAspGluAspValGluLysGluMetLeuAsnHis
                                                                                                                                                            GluAsnIleAspAsnAspGluGluSerGluIleAspProLeuSerGluThrCysSerSer
                                                                                                                                                                                                                 AspAspAspThrLeuPheThrIleAspValSerValProArgAspTyrGlyAsnGluThr
                                                                                                                                                                                                                                           GAAGGAGCTTTATTTATTTAGTGTGAACTTAACTGTTCCTGAAAATGTATCCCAGGTAACG
                                                                                                                                                                                                                                                                                                                         LeuIleProAlaHisAspLeuValSerThrLeuSerGlnThrThrGluGlnProGiuIle 373
                                                                                                                                                                                                                                                                                                                                                                               ArgIleLeuGlyLysIleLeuSerLeuProGluPheCysSerProAlaAspSerProArg
GluCysLysGluThrAlaThrAspAlaGlnGlyLysLeuSerPro
                          TTTAAAGCGCTGAATTATACTAGCGGGGAAAAAAAAATATCTCCT
                                                                              GGTGCAGAG---
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                                                                                                                                                                                                                                                                       LeuGlnThrProGluThrSerSerAlaThrAsnAspLeuIleAspGluAspSerAspLys 393
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                                                                                 -GTTACACCTAATCAACAAATAACT
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Search completed: April 10, 2006, 10:06:14 Job time : 186.5 secs

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-MODEL=frame+ n2p.model -DEV=xlp
-Q=/abse/ABSWEB spool/US10768093/runat 10042006 090307 4612/app_query.fasta_1
-Q=/abse/ABSWEB spool/US10768093/runat 10042006 090307 4612/app_query.fasta_1
-DB=Issued_PatenTs_AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=5its -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIGT=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_WIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-MOST=abse02p -USER=US10768093 @CGN 1 1 71 @runat 10042006 090307 46512 -NCPU=6
-ICPU=3 -NO MMAP -NEG SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG -DBV TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Listing first 45 summaries
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Ygapop 10.0 , )
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1. /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6. /cgn2_6/ptodata/1/iaa/Backfiles1.pep:*
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308
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Ygapext
Fgapext
Delext
US-09-107-532A-4742
US-09-323-872A-25
US-09-072-433-30
US-09-072-433-30
US-09-134-000C-6467
US-09-134-000C-6467
US-09-538-09-134-6955
US-09-543-681A-6955
US-09-543-681A-6955
US-09-248-796A-18392
US-09-248-796A-18392
US-09-248-796A-18392
US-09-248-796A-18392
US-09-248-796A-18392
US-09-248-796A-18392
US-09-248-796A-18392
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US-09-248-796A-18392
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Sequence
Sequence
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    25, Appl
14853, Appl
6467, Ap
314, App
21015, Ap
6955, Ap
6955, Ap
18392, Ap
4037, Ap
6866, Ap
23709, A
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-09-107-532A-4	-09-538-092-3	US-09-631-594-50	-09-103-331-4	-09-538-092-21	-09-328-352-6	-09-107-532A-716	-09-134-000C-67	8-983-045-4	-09-583-110-275	-09-270-767-4689	-09-270-767-316	-09-270-767-5290	-09-270-767-3769	-09-949-01	-09-949-016-607	-09-134-000C-4	-769-787-16	-09-919-497-5	-09-710-279-15	-09-107-532A-45	-09-328-352-50	8-913-477	-09-248-796A	-09-328-352-767	-08-913-477-	9-134-001C	-09-710-279-277	-09-134-000C-5	-10-270-085-	-09-723-820	9-541-782-	US-09-902-540-11397
4858	371	50,	41,	213	6069	7169	674	4,	275	4689	316	5290	3769	7359	6079	4976	164,	56,	154	Sequence 4564, Ap	5033	23,	175	767	21,	511	277	5020	2, 1	2, 1	2, 2	1139

ALIGNMENTS

US-09-107-532A-4742; Sequence 4742; Ap

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OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998.
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/ACENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
PRIEDENIC ACCOUNT NUMBER: 40,489
PRIEDENICA NUMBER: 40,489
                    REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES; 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 Beaver Street
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: (B) LOCATION 1...378 SEQUENCE DESCRIPTION: SEQ ID NO: 4742: US-09-107-532A-4742
                                                                                                                                                                                                                           US-09-323-872A-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
APPLICANT: Coschigano, Peter
TITLE OF INVENTION: Compositions and Methods for Bioremediation
FILE REFERENCE: OHU-03640
CURRENT APPLICATION NUMBER: US/09/323,872A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/072,433
PRIOR FILING DATE: 1998-05-04
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
SEQ ID NO 25
LENGTH: 740
                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                Sequence 25, Application US/09323872A Patent No. 6395539
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HYPOTHETICAL: YES
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                             ---GCGCTGAATTATACTAGCGGGGAAAAA 470
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CHARACTERISTICS:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                   COUNTRY:
                                                                                                                                                                                                   ADDRESSEE:
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; TYPE: PRT ; ORGANISM: Clostridium pasteurianum US-09-323-872A-25
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6551814
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30, Application US/09072433 Patent No. 6551814
           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Coschigano, Peter W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: BIOREMEDIATION
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             STREET:
STREET:
San F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450 AATTATACTAGCGGGAAAAAAAAATATCTCCTGGAATATATAACGAT---CAGGTTATG 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     405 CysCysValSerAlaMetArgValGlyLysAspMetGlnPheGlyAlaArgCysAsn 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 IleGinTyrGluAsnAspAspIleMetArgProIleTyrGlyAspAspTyrAlaIleAla 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 HisThrLeuIleAsnLeuGlySerAlaProGluProAsnMetThrValLeuTrpSerGlu 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 ACGACTATTTCAAAAAGTTTTTTTGCACCTGAACCACGAATACAGCCTTCTTTTGGTGAA 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTGCTTCATTCGGCAGCCATGCCAGAACAGAAATAGCGACTAAAAACTTCCCAGTATCA 152
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                                                                                                                                                                                                    California
                                                                                                                                                                                                                                               E: Medlen & Carroll, LLP
220 Montgomery Street, Suite 2200
                                                                                                                                                                                 United States
                                                                                                                                                                                                                              Francisco
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38.6%
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US/09/072,433
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US-09-248-796A-14853
Sequence 14853, Application US/09248796A
Parent NO. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AM:
TITLE OF INVENTION: FOR DIAGNOSTICS AND
FILE REFERENCE: 107196.132
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Best Local Similarity:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 740 amino acids
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATGTTGGAAAGGAAGGAGCTTTATTATTTAGTGTGAACTTAACTGTTCCTGAAAATGTA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTGCTTCATTCGGCAGCCATGCCAGAACAGAAATAGCGACTAAAAACTTCCCAGTATCA 152
                                                                                                                                                                                                                                                                                            AATTATACTAGCGGGGAAAAAAAATATCTCCTGGAATATAAAAGAT---CAGGTTATG
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Mismatches:
Indels:
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Matches:
                    AMINO ACID SEQUENCES RELATING AND THERAPEUTICS
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC
TITLE OF INVENTION: ENTERCOCCUS FAECALIS FO.
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055;778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 6467
LENGTH: 768
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Best Local Similarity:
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PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14853
                                                                                                                                                                                                                                                                                                          Sequence 6467, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATACCGCTGATGCTTCCCAATCAATAATCTACCAGATTGTTGATGAGAAAGGGGAAAAAA 389
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Matches:
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Mismatches:
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Percent Similarity:
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Query Match:
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APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR PRICING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR PILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
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US-09-134-000C-6467
                                                                                                                                                                                                                                                                      Sequence 314, Application Patent No. 6753314
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HisPheAsnPheGluTyrAspGlnAlaLeuIleGlnGlnLeuTyrAspGluGlnSerGlu 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuTyrArgArgTyrLeuAlaLysGluTyrGlyLysArgLysGlnMetValSerGlyIle 156
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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SEQ ID NO 314
LENGTH: 345
                                                                                                                                                                                                 Sequence 21015, Appropriate No. 6551795
                              FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
       PRIOR APPLICATION NUMBER:
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                                                                                      Percent Similarity:
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; ORGANISM: Proteus mirabilis
US-09-543-681A-6955
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; TYPE: PRT
; ORGANISM: Pseudomonas
US-09-252-991A-21015
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PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21015
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LENGTH: 186
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
UNMBER OF SEQ ID NOS: 8344
                                                                    Local Similarity:
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x US-09-543-681A-6955 (1-186)
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CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18392
LENGTH: 308
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                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18392, Application US/09248796A Patent No. 6747137
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ORGANISM: Candida
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                                                                                        37 MetThrArgGlnSerLeuLeuThrProThrLysThrAspTyrSerAspAlaHisGlyAsn
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                                                                                                                         TTGACACATTACGAATGTTATGTATACAATAAAAATGATTATAGCAATATTAATGGTGT-
                  SerGluGlyAlaGlnGlnTyrLysGluLysTrpIleLysIle-
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RESULT 10
US-09-134-001C-4037
; Sequence 4037, Ap
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT PILLING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4037
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GGAGCTTTATTATTTAGTGTGAACTTAACTGTTCCTGAAAATGTATCCCAGGTAACGGTC
                                       TyrPheGluGlnThrGluValArgLeuValLeuSerPheLeuArgThrIleAspAsnPro
                                                                                TTTTTT----GCACCTGAACCACGAATACAGCCTTCTTTTGGTGAAAATGTTGGAAAGGAA
                                                                                                                     AsnLeuGlnGlnAlaPheLysAsnAsnAspIleProPheHisValAsnSerLysGluGly
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GENERAL INFORMATION: MICHEIC ACID AND AMINO ATITLE OF INVENTION: NUCLEIC ACID AND AMINO ATITLE OF INVENTION: BAUMANNII FOR DIAGNOSTION: BAUMANNII FOR DIAGNOSTION: PILE REFERENCE: GTO99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 6886

LENGTH: 218
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Best Local Similarity:
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US-09-328-352-6886
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Patent No. 6562958
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                                                                                                                                         AlaGlyAspValAlaGlyArgThrProPheGlnIleAsnLeuThrAsnCysAlaSerVal 119
                                                                                                                                                                              GTTGGAAAG---GAAGGAGCTTTATTATTTAGTGTGAACTTAACTGTTCCTGAAAATGTA 272
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                                                               GlyLysValAlaThrTyrPheGluProGlyAlaThrValAspPheAsnThrGlyArgLeu 139
                                                                                                                                                                                                                                                             ACTATTTCAAAAAGTTTTTTTGCACCTGAACCACGAATACAGCCTTCTTTTGGTGAAAAT 215
                                                                                                                                                                                                                                                                                                  AlaAlaAspGlyThrIleThrIleAsnGlyLeuValThrAspAsnThrCysThrIleAsp 79
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                                                                                                                                                                                                                      ThrGlyAspLysAsnLeuThrValAsnLeuProThrValSerSerGlnSerLeuLysAsn 99
                                                                                                      TCCCAGGTAACGGTCTAC-----CCTGTTTATGATGAAGATTATGGGTTAGGACGACTA 326
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    ACCGCTGATGCTTCCCAATCAATAATCTACCAGATT---
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23709
LENGTH: 527
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US-09-252-991A-23709
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Sequence 11397, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: GOLdman, Barry S.
APPLICANT: Hinkle, Gregory J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 107196.136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 GlyValLeuLeuValMetAlaArgPheArgArgIleLeuGluIleAspProLeuGlyArg 148
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                                                                                                                                                                   LeuGlnValAspIleValThrLeuGluGlyGluArgLeuSerLeuGly 223
                                                                                                                                                                                                                                                                                                                                                                                                               PheAlaArgValGlnProGlyValArgAsnLeuAlaIleSerGlnAlaAlaAlaProHis 168
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                                                                                                                                                                                                           TCCCAGGTAACGGTCTACCCTGTTTATGATGAAGATTATGGGTTAGGA 320
                                                                                                                                                                                                                                               AlaGluAsnAlaGlyGlyValHisCysLeuLysTyrGlyLeuThrVal---HisAsnLeu
                                                                                                                                                                                                                                                                                        GGAAAGGAA-----GGAGCTTTATTATTTAGTGTGAACTTAACTGTTCCTGAAAATGTA 272
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                                                               Alignment Scores
                                                                                                            TYPE: PRT
ORGANISM: A. nidulans
US-09-541-782-2
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                                                Pred. No.:
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SEQ ID NO 2
LENGTH: 11
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LENGTH: 603
TYPE: PRT
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APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                             APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
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CURRENT APPLICATION NUMBER: US/09/723,820
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/41,782
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; ENGTH: 1184
; TYPE: PRT
; ORGANISM: A. nidulans
US-09-723-820-2
                                    Percent Similarity:
Beet Local Similarity:
Query Match:
DB:
US-10-768-093-4 (1-527) x US-09-723-820-2 (1-1184)
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US-09-723-820-2
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PPLICANT: Nislow, Corey

PPLICANT: Sakowicz, Roman

PPLICANT: Beraud, Christophe

TITLE OF INVENTION: Antifungal Assay

ILE REFERENCE: 1015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTCCTGAAAATGTATCCCAGGTAACGGTCTACCCTGTTTATGATGAAGATTATGGGTTA 317
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Matches:
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PheArgAlaLysAsnIle 416	AGCGGGGAAAAAAAATA 476	:::::: AlaThrMetSerProAlaArgSerAsnLeuGluGluThrIleSerThrLeuAspTyrAla 410	PATACT	SerLysLeuThrArgLeuLeuGlnAspSerLeuGlyGlyArgThrLysThrCysIleIle 3	[AAAAGATCATGGT	GlyArgValIleAsnAlaLeuValAspLysSerGlnHisIleProTyrArgGlu 3	TTGTTGAT	GluAsnLysArgAlaThrGluAlaGlyLeuIleAsnLysSerLeuLeuThrLeu 3	GTTCCTGAAAATGTATCCCAGGTAACGGTCTACCCCTGTTTATGATGAAGATTATGGGTTA 3	LeuAlaGlySerGluAsmIleGlyArgSerGlyAla3	TATTTAGTGTGAACTTAACT	LysArgThrThrGluSerGlyGluGluTyrValCysProGlyLysLeuAsnLeuValAsp 3		ThrLysCysAsnAspLeuSerSerArgSerHisThrValPheThrIleThrValAsnIle		ThralaGlyIleLysLeuLeuGlnGlnGlySerHisLysArgGlnValAlaAla	ACAATTGGTTTAATTCTAATTCTTGCTTCATTCGGCAGCCATGCCAGAACAGAAATAGCG 1
		011	458	390	407 •	370	374	352	317	334	257	322	200	302	161	282	131

Search completed: April 10, 2006, 10:08:36 Job time : 38.5 secs

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Command line parameters:

-MODEL-frame+ n2p.model -DEV=xlp
-Q=/abse/ABSSWEB spool/US10768093/runat_10042006_090309_4677/app_query.fasta_1
-Q=-Abse/ABSSWEB spool/US10768093/runat_10042006_090309_4677/app_query.fasta_1
-DB=Published_App_lications_AA_Main -QFMT=fastan -SUFFIX=n2p.rapbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=blits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DCLIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-THR MAX=100 -THREN=0 -MAXLEN=2000000000 -HOST=abse02p
-USER=JUS10768093_@CGN_1 1_307_@xrunat_10042006_090309_4677 -NCPU=6 -ICPU=3
-NO MMAAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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seq length: 2000000000
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Ygapop 10.0 , Y
Fgapop 6.0 , I
Delop 6.0 , I
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1: /cgn2_6/ptodate/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodate/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodate/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodate/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodate/1/pubpaa/US10B_PUBCOMB.pep:*
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8.91.31
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Ygapext
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US-10-768-093-10
US-10-197-666A-100
US-10-282-122A-77158
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US-10-768-093-6
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US-10-754-641-5
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10-369-493-2489
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Sequence 9, Appli
Sequence 9, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 10, Appl
Sequence 100, Appl
Sequence 7158, A
Sequence 2489, Appl
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-11-097-143-429	-10-437-963-1511	-10-450-763-48573	-10-369-493-2355	-10-724-972A-603	2-122A-609	-10-282-122A-544	-10-282-122A-5862	-09-815-242-11	-10-282-122A-446	-10-282-122A-7050	-10-470-048B-44	-10-282-122A-6731	-10-282-122A-68	-10-369-493-2138	-10-389-647-66	-10-437-963-13	0-724-972A-584	-10-452-024-7	-10-741-849-709	-09-815-242-11936	-10-425-115-223	-10-282-122A-6697	-10-197-666A-9	-10-001-21	-10-311-034-	-10-197-666A-9	-10-197-666A-9	-10-369-493-1743	-10-437-963-161	-10-501-282-398	-10-424-599-25071	-10-424-599-1901	US-10-357-567-25
equence 429	equence 151131,	nce 48573	equence 23554,	equence 6030,	equence 6095	equence 54471,	equence 58624,	equence 11293,	equence 44691,	equence 70506,	equence 444, A	equence 6731!	equence 68607,	equence 21384,	equence 664, Ap	equence 136628,	equence 5848, A	equence 76, App	equence 7096	equence 11936,	equence 2237	equence 66978,	equence 98, Ap	equence 2, Appl	equence 8, Appl	equence 96, App	equence 94, App	equence 17433,	equence 1616	equence 3988	equence 25071	equence 190153	equence 25, A

ALIGNMENTS

RESULT 1 US-10-768-093-5

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Sequence 5, Application US/10768093 Publication No. US20040156829A1 GENERAL INFORMATION:
                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/768,093
FILING DATE: 02-Feb-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                NAME: Hendricks, Glenna M
REGISTRATION NUMBER: 32,535
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                            ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                            ATTORNEY/AGENT INFORMATION: NAME: Hendricks, Glenn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cassels, Fred J
Boedeker, Edgar C
TITLE OF INVENTION: Transformed Bacteria Producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wolf, Marcia K
                                                                                                       APPLICATION NUMBER: US/09/479,877B FILING DATE: 10-Jan-2000
                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Fairfax
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. Box 2509
TELEPHONE: 703/425-8405
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
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Sequence 5, Application US/10754641

Publication No. US20050025787A1

GENERAL INFORMATION:
APPLICANT: U.S. Army Medical Research and Materiel Complicant: Wolf, Marcia K.
APPLICANT: Wolf, Marcia K.
APPLICANT: Wolf, Marcia K.
APPLICANT: Boedeker, Edgar C.
APPLICANT: Boedeker, Edgar C.
FITLE OF INVENTION: TRANSFORMED BACTERIA PRODUCING CS6
FILE REFERENCE: 034047.033 3
CURRENT APPLICATION NUMBER: US/10/754,641
CURRENT FILING DATE: 2004-01-12
PRIOR APPLICATION NUMBER: 09/479,877
PRIOR APPLICATION NUMBER: 08/48,145
PRIOR APPLICATION NUMBER: 08/78,145
PRIOR FILING DATE: 1997-01-24
PRIOR APPLICATION NUMBER: 08/243,482
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
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SEQ ID NO: 5:
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Conservative:
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Indels:
Gaps:
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Percent Similarity:
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Query Match:
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US-10-768-093-9
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US-10-754-641-5
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NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 154
TYPE: PRT
                                                                                                                                                                                                                                             Sequence 9, Application US/10768093
Publication No. US20040156829A1
GENERAL INFORMATION:
APPLICANT: Wolf, Marcia K
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                      NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and
                                                                                                                                                                                                  Cassels, Fred J
Boedeker, Edgar C
TITLE OF INVENTION: Transformed
                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnIleValAspGluLysGlyLysLysMetLeuLysAspHisGlyAlaGluValThrPro
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83.6%
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US-10-754-641-9
; Sequence 9, Application US/10754641
; Publication No. US20050025787A1
; GENERAL INFORMATION:
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DB:
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Best Local Similarity:
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APPLICANT: U.S. Army Medical Research and Materiel Command APPLICANT: Wolf, Marcia K.
APPLICANT: Cassels, Frederick J.
APPLICANT: Boedeker, Edgar C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hendricks, Glenna M
REGISTRATION NUMBER: 32,535
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/425-8405
TELEFAX: 703/425-8406
ORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 136 amino acids
TYPE: Amino acid
STRANDEDNESS; single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/768,093
PILING DATE: 02-Feb-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/479,8778
APPLICATION NUMBER: US/09/479,8778
FILING DATE: 10-Jan-2000
ATTORNEY/AGENT INFORMATION:
NUMBE: Hendricks, Glenna M
NUMBE: Hendricks, Glenna M
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Matches:
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Query Match:
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                                                                                                                                                       Sequence 6, Application US/10768093
Publication No. US20040156829A1
PUBLICANTION:
APPLICANT: Wolf, Marcia K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn SEQ ID NO 9
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NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/479,877
PRIOR FILING DATE: 2000-01-10
PRIOR APPLICATION NUMBER: 08/788,145
PRIOR FILING DATE: 1997-01-24
PRIOR APPLICATION NUMBER: 08/243,482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/754,641
CURRENT FILING DATE: 2004-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: TRANSFORMED BACTERIA PRODUCING CS6 ANTIGENS FILE REFERENCE: 034047.033.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Escherichia coli
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                                                                  Cassels, Fred J
Boedeker, Edgar C
TITLE OF INVENTION: Transformed
Antigens as
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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            CITY: Fairfax
STATE: VA
                                     ADDRESSEE: Hendricks and Assoc
STREET: P.O. Box 2509
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
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Indels:
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Vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hendricks, Glenna M
REGISTRATION NUMBER: 32,535
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 703/425-8405
TELEFAX: 703/425-8406
INFORMATION FOR SEQ ID NO: 6:
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FILING DATE: 02-Feb-2004
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION NUMBER: US/09/479,8778
APPLICATION NUMBER: US/09/479,8778
FILING DATE: 10-Jan-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACEBATIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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                                                                                   393
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  GluAsnThrSerTyrThrPheSerAlaIle---TyrThrGlyGlyGluTyrProAsnSer 149
                                                                                                                                                                                                ACGGTCTACCCT------GTTTATGATGAAGATTATGGGTTAGGACGACTAGTAAAT 332
                                                                                                                                                                                                                                                       AAGGAAGGAGCTTTATTATTTAGTGTGAACTTAACTGTTCCTGAAAATGTATCCCAGGTA 281
                                                                                                                                                                                                                                                                                                                                         AsnAlaGlyAsnTrpGlnTyrLysSerLeuAspValAsnValAsnIleGluGlnAsnPhe 39
                                                                                                                                                                                                                                                                                                                                                                     GAAATAGCGACT-----AAAAACTTCCCAGTATCAACGACTATTTCAAAAAGTTTT 173
                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAAGAAAACAATTGGTTTAATTCTAATTCTTGCTTCATTCGGCAGCCATGCCAGAACA 122
                      CCTAATCAACAAATAACTTTTAAAGCGCTGAATTATACTAGCGGGGAA-----AAA 470
                                                        ArgLysAspSerGlyAlaGlyAsnPheMetAlaGlyGlnLysGlySerPheProValLys 130
                                                                                    TTAAAAGATCATGGTGCA----
                                                                                                                                        Ile --- ProAspIleAspSerAlaValArgIleIleProValAsnTyrAspSerAspPro 58
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                                                                                                                                                                    LysIleAlaProThrAspSerLeuThrSerSerGlyGlnGlnIleGlyLysLeuValAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 167 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                               ValAsnAsnProAspGlnAsnMetAsnTyrTyrIle-----
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Pred. No.:
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Query Match:
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PRIOR FILING DATE: 2000-01-10
PRIOR APPLICATION NUMBER: 08/78,145
PRIOR FILING DATE: 1997-01-24
PRIOR APPLICATION NUMBER: 08/243,482
PRIOR FILING DATE: 1994-05-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.2
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-768-093-4 (1-527) x US-10-754-641-6 (1-167)
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TYPE: PRT
; ORGANISM: Escherichia coli
US-10-754-641-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wolf, Marcia K.
APPLICANT: Cassels, Frederick J.
APPLICANT: Boedeker, Edgar C.
TITLE OF INVENTION: TRANSFORMED BACTERIA PRODUCING
FILE REFERENCE: 034047.033.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: U.S. Army Medical Research and Materiel Command APPLICANT: Wolf, Marcia K.
APPLICANT: Cassels, Frederick J.
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CURRENT FILING DATE: 2004-01-12
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131 GluAsnThrSerTyrThrPheSerAlaIle---TyrThrGlyGlyGluTyrProAsnSer 149
                                                                                                                                                                                                                                                                                                                                                      282 ACGGTCTACCCT------GTTTATGATGAAGATTATGGGTTAGGACGACTAGTAAAT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 ATGAAGAAAACAATTGGTTTAATTCTAATTCTTGCTTCATTCGGCAGCCATGCCAGAACA 122
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2 LeuLysLysIleIleSerAlaIleAlaLeuIleAla-----GlyThrSerGlyValVal 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnAlaGlyAsnTrpGlnTyrLysSerLeuAspValAsnValAsnIleGluGlnAsnPhe 39
                                       CCTAATCAACAATAACTTTTAAAGCGCTGAATTATACTAGCGGGGAA------AAA 470
                                                                                                                                                    TTAAAAGATCATGGTGCA----
                                                                                                                                                                                                    ValAsnAsnProAspGlnAsnMetAsnTyrTyrIle---
                                                                                                                                                                                                                                                 ACCGCTGATGCTTCCCAATCAATAATCTACCAGATTGTTGATGAGAAAGGGGAAAAAAATG 392
                                                                                                                                                                                                                                                                                                   LysIleAlaProThrAspSerLeuThrSerSerGlyGlnGlnIleGlyLysLeuValAsn 98
                                                                                                                                                                                                                                                                                                                                                                                                   AAGGAAGGAGCTTTATTATTTAGTGTGAACTTAACTGTTCCTGAAAATGTATCCCAGGTA 281
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                                                                                                    ArgLysAspSerGlyAlaGlyAsnPheMetAlaGlyGlnLysGlySerPheProValLys 130
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Percent Similarity:
Best Local Similarity:
Query Match:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            NO .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hendricks, Glenna M
REGISTRATION NUMBER: 32,535
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/425-8406
TELEFAX: 703/425-8406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/479,877B
FILING DATE: 10-Jan-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENELIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Boedeker, Edgar C
TITLE OF INVENTION: Transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wolf, Marcia K
                                 243
                                                                                                             135 AAAAACTTCCCAGTATCAACGACTATTTCAAAAAGTTTTTTTGCACCTGAA-----
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45 ThrValGluMetThrIleProAlaGlyValSerAlaValLysIleAlaProThrAspSer 64
                                                                       25 AlaValArgIleIleProValAsnTyrAspSerAspProLysLeuAspSerGlnLeuTyr 44
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                                 AGTGTGAACTTAACTGTTCCTGAAAATGTATCCCAGGTAACGGTCTACCCT-----
                                                                                                                                              APPLICATION NUMBER: US/10/768,093
FILING DATE: 02-Feb-2004
CLASSIFICATION: <Unknown>
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113.50
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SEQ ID NO 100
LENGTH: 911
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TITLE OF INVENTION: Elk1 phosphorylation related
FILE REFERENCE: PH-1548US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/350,027 PRIOR FILING DATE: 2002-01-23 NUMBER OF SEQ ID NOS: 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: JP 2001-263450
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: JP 2002-012176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 ATAATCTACCAGATTGTTGATGAGAAAGGGGAAAAAAATGTTAAAAGATCATGGTGCA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      492 AACGATCAGGTTATGGTTACTATGTAAAC 524
                                                                                                                                                                    34 MetThrGlyTyrGlySerHisSerLysValTyrSerGlnSerLysAsnIleProLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 GluGlnThrIleValPheProGlySerThrGlyHisIleValValThrSerAlaSerSer 93
                                                                                             54 GlnProAlaThrThrValSerThrSerLeuProValProAsnProSerLeuProTyr 73
                                                                                                                                                                                                          93 CTTGCTTCATTCGGCAGCCATGCCAGAACAGAAATAGCGACTAAAAACTTCCCAGTATCA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 AsnPheMetAlaGlyGlnLysGlySerPheProValLysGluAsnThrSerTyrThrPhe 116
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9.3%
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                                                       CCTTCTTTTGGTGAAAATGTTGGAAAGGAAGGAGCTTTATTA 239
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                                  Alignment Scores
                                                                       ; LENGTH: 541
TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77158
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                                                                                                                                             Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614 SOFWARE: Patentin version 3.1 EQ ID NO 77158
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URRENT APPLICATION NUMBER: US/10/282,122A
URRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23
                                                                                                                                                                                                                      APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/267,636 FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICATION NUMBER: 60/207,727 ILING DATE: 2000-05-26
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Zamudio, Carlo
Malone, Cheryl
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Zyskind, Judith
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Forsyth, R.
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Trawick, John
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   Alignment Scores: Pred. No.:
                                                        ; TYPE: PRT ; ORGANISM: Schizosaccharomyces US-10-369-493-2489
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                                                                                                                             CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2489
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2489, Application US/10369493 Publication No. US20030233675A1
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Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
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; Sequence 25, Application US/10267989

; Publication No. US20030199035A1
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Percent Similarity:
Best Local Similarity:
; TYPE: PRT
; ORGANISM: Clostridium
US-10-267-989-25
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                                                                                                             CURRENT APPLICATION NUMBER: US/10/267,989
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US/08/981,097
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: PCT/DK97/00336
PRIOR FILING DATE: 1997-08-20
PRIOR APPLICATION NUMBER: 08/701,458
PRIOR APPLICATION NUMBER: 08/701,458
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 44
                                                                          SOFTWARE: PatentIn version 3.0 SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            APPLICANT: MADSEN, Soeren
TITLE OF INVENTION: METABOLICALLY ENGINEERED LACTIC ACID BACTERIA
TITLE OF INVENTION: MEANS FOR PROVIDING
TITLE OF INVENTION: SAME
FILE REFERENCE: ARNAU-1A
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                                                         LENGTH: 740
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JOERGENSEN, Flemming
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                                                                                                 NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3
SEQ ID NO 25
LENGTH: 740
TYPE: PRT
ORGANISM: Clostridium paster
US-10-357-567-25
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Best Local Similarity:
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    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-357-567-25
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Publication No. US20040038382A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/046,845 PRIOR FILING DATE: 1997-05-05
                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/357,567
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/072,433
PRIOR FILING DATE: 1998-05-04
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Coschigano, Peter TITLE OF INVENTION: Compositions and Methods FILE REFERENCE: OHU-07748
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Best Local Similarity:
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                                                                    Percent Similarity:
                                                                                                                      Alignment Scores:
                                                                                                                                                           ) OTHER INFORMATION: US-10-424-599-190153
                                                                                                                                                                                                                                                               TITLE OF INVENTION: Soy Nucleic Acid Molec
TITLE OF INVENTION: Plants and Uses There
FILE REFERENCE: 38-21(5223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEO ID NOS: 285684
SEO ID NO 190153
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
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; Sequence 250712, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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                                                                                                                          US-10-768-093-4 (1-527) x US-10-424-599-250712
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                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 250712
LENGTH: 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid
TITLE OF INVENTION: Plants and Uses
FILE REFERENCE: 38-21(53223)B
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APPLICANT: Kovalic David
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ORGANISM: Glycine
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                                                                                        CAATATTAATGGTGTTATATGAAGAAAACAATTGGTTTAATTCTAATTCTTGCTTCATTC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluLeuTyrGlnLeuLysAspLysLeuGly 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaAsnCysThrPheArgGlyValSerAspLysGlyValValLeuValLeuProAlaPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluAlaAspGluGlyLysGluAspPheIleValTyrGlyValAsnLeuThrPhe----Val
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheLeuValLeuSerLysIleGluAlaAspPheSerThrGlyLysTyrGluIleSerGlu 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCCAGTATCAACGACTATTTCAAAAAGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTAATTCTAATTCTTGCTTCATTCGGCAGCCATGCCAGAACAGAAATAGCGACTAAAAAC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTTATGATGAAGATTATGGGTTAGGACGACTAGTAAATACCGCTGATGCTTCCCCAATCA 353
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38.4%
23.9%
8.8%
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                                                                                                                                                                                                                                                                                                                       ID: PAT_MRT3847_68422C.1.pep
                                                       -HisArgThrLeuHisLysAsnAlaProSerThrIlePhe 34
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Matches:
Conservative:
                                                                                                                                                                                Mismatches:
Indels:
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Thereof for Plant Improvement
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Score:

AAGGAAGGAGCTTTATTATTTAGTGTGAACTTAACTGTTCCT 263	Qy 213 AATGTTGGAAAGGAAGGAGCTT
ACGACTATTTCAAAAAGTTTTTTTGCACCTGAACCACGAATACAGCCTTCTTTTGGTGAA 212	Oy 153 ACGACTATTTCAAAAAGTTTTTTTGCACCTY
	Oy 93 CTTGCTTCATTCGGCAGCCATGCCAGAACAC
501-282-3988 (1-750)	US-10-768-093-4 (1-527) x US-10-501-282-3988
Length: 750 Matches: 38 Conservative: 32 Mismatches: 61 Indels: 36 Gaps: 8	Alignment Scores: Pred. No.: Score: 83.00 Matchi Percent Similarity: 11.9% Best Local Similarity: 22.8% Ouery Match: 8.8% Gaps:
GAACCACGAATACAGGCTTCTTT	NNT: 0 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0
AsnAsnHisGlyThrArqLysAsnAlaTrpProThrSerLeuLeuProLeuAlaLeuAla 54	Db 35 AsnAsnHisGlyThrArgLysAsnAlaTrp

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504 ATGGTTGGTTACTATGTAAAC 524
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482 LeuAlaGlyLeuTyrIleAsn 488
                                       468 TyrAspGluValValGluLysTyr-----
                                                           453 TATACTAGCGGGGAAAAAAAATATCTCCTGGAATATATAACGATCAGGTT------ 503
                                                                             345 TCCCAATCAATAATCTACCAGATT------GTTGATGAGAAAGGGGAAAAAATGTTA 395
                                                                                                                                                           |||:::
415 CysValSerAlaMetGluIleGlyLysGlnMetGlnPhePheGlyAlaArgAlaAsnLeu 434
                                                                                                                                                                              324 CTAGTAAATACC------GCTGATGCT 344
                                                                                                                                                                                                  ----AspGlnMetThrGluTrp 481
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Search completed: April 10, 2006, 10:12:53 Job time : 129.5 secs

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Regult
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-MODEL-strame+ nip.model DEV=xlp
-Q-/abse/ABSWEB spool/US10768093/runat 10042006 090311 4719/app query.fasta 1
-Q-/abse/ABSWEB spool/US10768093/runat 10042006 090311 4719/app query.fasta 1
-DB=Published Applications AA New -QFMT=fastan -SUFFIX=nip rapbn -MINMATCH=0.1
-LOOPECL=0 -LOOPEXT=0 -UNITS-bIts -START=1 -END=-1 -MATRIX=blosum62
-TRAMS=human40.cdi -LIST=45 -DCALIGN=200 -THR SCORE=pct -THR MXX=100
-TRAMS=human40.cdi -LIST=45 -DCALIGN=200 -THR SCORE=pct -THR MXX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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-USER=US10768093 @CGN 1 1 25 @runat 10042006 090311 4719 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 "WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
       0 W A D D C B D
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   90.5
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                                                                                                                                                                                                                                                                                                                                          Published Applications AA_New:*

1: /SIDSS/ptodata/2/pubpaa/USOS_NEW_PUB.pep:*

2: /SIDSS/ptodata/2/pubpaa/USOS_NEW_PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDSS/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

6: /SIDSS/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

7: /SIDSS/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

8: /SIDSS/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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length: 2000000000
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Match
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939
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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     GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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   268
379
416
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1198
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     6776677
US-11-195-739-6
US-11-096-568A-6312
US-11-096-568A-6311
US-11-096-568A-6310
US-10-451-375-4
US-10-451-375-3
US-11-096-568A-32647
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                 Sequence 6,
Sequence 631
Sequence 631
Sequence 4,
Sequence 3,
Sequence 3,
Sequence 3,26
Sequence 3,26
                                                                                                                                                                                    Description
   6, Appli
6312, Ap
6311, Ap
6310, Ap
4, Appli
3, Appli
3, Appli
3, Appli
32647, A
32646, A
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a

ALIGNMENTS

RESULT 1 US-11-195-739-6

Sequence 6, Application US/11195739
Publication No. US20060019324A1
GENERAL INFORMATION:

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APPLICANT: ALZARI, PEDRO
APPLICANT: BOITEL, BIRGITTE
APPLICANT: HOLLARINO, ANDREA.
APPLICANT: FERNANDEZ, PABLO
APPLICANT: FERNANDEZ, PABLO
APPLICANT: FERNANDEZ, PABLO
APPLICANT: FERNANDEZ, PABLO
APPLICANT: FERNANDEZ, PABLO
APPLICANT: COLE, STEWART
TITLE OF INVENTION: INHIBITORY SUBSTANCES
FILE REFERENCE: 252853US
FILE REFERENCE: 252853US
CURRENT APPLICATION NUMBER: US/11/195,739
CURRENT APPLICATION NUMBER: US/11/195,739
CURRENT FILING DATE: 2005-08-03
PRIOR APPLICATION NUMBER: US/10/892,170
PRIOR APPLICATION NUMBER: US/10/487,943
PRIOR APPLICATION NUMBER: US/10/487,943
PRIOR FILING DATE: 2003-07-18
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US/10/487,943
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US/10/487,943
PRIOR FILING DATE: 2003-07-18
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PRIOR APPLICATION NUMBER: US/
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Alignment :
Pred. No.:
                                                                                                                      FEATURE:
NAME/KEY: misc feature
LOCATION: (1). (379)
OTHER INFORMATION: Ceres Seq.
US-11-096-568A-6312
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 Query Match:
DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 6312
LENGTH: 379 .
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6312, Application US/11096568A Publication No. US20060048240A1
                                                                                                                                                                                                                                                                              APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
                                                                                                                                                                                                   ORGANISM: Glycine max
                                                                                                                                                                                                                     TYPE: PRT
                                                                                           Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerGlnGluProGluAlaGluThrThrValGlyAlaGlyGlnSerValThrLeuThrVal 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAAATGTTGGAAAGGAAGGAGCTTTATTATTTAGTGTGAACTTAACTGTTCCTGAAAAT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAACGACTATTTCAAAAAGTTTTTTTGCACCTGAACCACGAATACAGCCTTCTTTTGGT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyThrValIleThrThrLysProAlaProGlyGluLysAlaAsnArgGluGluSerVal
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                Conservative: Mismatches: Indels:
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Sequence 6311, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined
TITLE OF INVENTION: There
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                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 6311
LENGTH: 416
                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: (1)..(416) OTHER INFORMATION: Cer
                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Glycine max
FEATURE:
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                                               ValValThrileCysThrSerGluSerAsnArgAlaGluAsnGluPheProThrAsnGly 282
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NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 6310

LENGTH: 450

TYPE: PRT

ORGANISM: Glycine max
PEATURE:
PATURE:
LOCATION: (1)...(450)

OTHER INFORMATION: Ceres Seq. ID no
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Best Local Similarity:
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Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
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GluAlaAspGluGlyLysGluAspPheIleValTyrGlyValAsnLeuThrPhe---Val 375
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                                                                    LeuValLysLeuIleAlaGluAsnLysMetValGluAsnHisValMetGluLysLeuVal 356
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                                                                                                      -----TTTGCACCTGAACCACGAATACAGCCTTCTTTTGGTGAAAATGTT--- 218
                                                                                                                                    PheLeuValLeuSerLysileGluAlaAspPheSerThrGlyLysTyrGluIleSerGlu
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Best Local Similarity:
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US-10-451-375-4
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US-10-451-375-4
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Publication No. US20050261482A1
GENERAL INFORMATION:
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TITLE OF INVENTION: REGULATION OF HUMAN SERINE-THREONINE PROTEIN KINASE
FILE REFERENCE: LIO264 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/451,375
CURRENT FILING DATE: 2003-07-02
PRIOR APPLICATION NUMBER: US 60/259,215
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/306,468
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/308,098
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 14
SOPTMARE: Patentin version 3.1
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ThrSerValThrGlyGlnValLeuGlyGlyProHisAsnLeuMetArgArgSerThrVal 120
                                                                                                                                                                                         GluGlnThrIleValPheProGlySerThrGlyHisIleValValThrSerAlaSerSer 100
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                                                    SerLeuLeuAspThrTyr---GlnLysCysGlyLeuLysArgLysSerGluGluIleGlu
                                                                                        ACGGTCTACCCTGTTTATGATGAAGATTATGGGTTAGGACGACTAGTAAATACCGCTGAT 341
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Matches:
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Pred. No.:
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US-10-451-375-3
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Publication No. US20050261482A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: US 60/306,468
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/308,098
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: REGULATION OF HUMAN SERINE-THREONINE PROTEIN KINASE FILE REFERENCE: LIO264 Foreing Countries CURRENT APPLICATION NUMBER: US/10/451,375
CURRENT FILING DATE: 2003-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
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|GlnProAlaSerThrThrValSerThrSerLeuProIleProAsnProSerLeuProTyr 73
                                                                                                        ### ABNThrSerSerVal-----GlnIleIleGluGluHis---ProProMetIleGlnAsn 149
                                                                                                                                            ACGGTCTACCCTGTTTATGATGAAGATTATGGGTTAGGACGACTAGTAAATACCGCTGAT 341
                                                                                                                                                                                                                                                    ThrSerValThrGlyGlnValLeuGlyGlyProHisAsnLeuMetArgArgSerThrVal 113
                                                                                                                                                                                                                                                                                                                            GluGlnThrIleIlePheProGlySerThrGlyHisIleValValThrSerAlaSerSer 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTGCTTCATTCGGCAGCCATGCCAGAACAGAAATAGCGACTAAAAACTTC-----
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GGGGAAAAAAAATATCTCCTGGAATATAT 491
                                    AsnAlaSerGlyAlaThrValAlaThrAlaThrThrSerThrAlaThrSerLysAsnSer
                                                                      CATGGTGCAGAGGTTACACCTAATCAACAATAACTTTTAAAGCGCTGAATTATACTAGC
                                                                                                                                                                              SerLeuLeuAspThrTyr---GlnLysCysGlyLeuLysArgLysSerGluGluIleGlu 132
                                                                                                                                                                                                                                                                                          TTTAGTGTGAAC-----TTAACTGTTCCTGAAAATGTA----TCCCAGGTA 281
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                                                                                                                                                                                                                    Sequence 32646, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
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SEQ ID NO 32647
LENGTH: 356
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 32647, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
                                                                                       CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 32646
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TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 205-04-01
                                                                                                                                                           TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVENTION: Therby FILE REFERENCE: 2750-1592PUS2
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LOCATION: (1)..(356)
OTHER INFORMATION: Ceres
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NAME/KEY: misc_feature
                      FEATURE:
                                LENGTH: 361
TYPE: PRT
ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTAATCAACAATAACTTTTAAAGCGCTGAAT---
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                                                                  Alignment Scores:
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                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 362
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                   APPLICANT: ESteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: ECT/US03/19153
PRIOR FILING DATE: 2003-6-16
PRIOR APPLICATION NUMBER: ECT/US03/19153
PRIOR FILING DATE: 2003-6-16
PRIOR APPLICATION NUMBER: E0/389,299
PRIOR FILING DATE: 2002-66-14
                                                                                                                                                                                 LENGTH: 1680
TYPE: PRT
ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                            FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(26)
                                                                                                                                                                     OTHER INFORMATION: Obtained
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Healey, Shaun
Hazlewood, Geoff
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DB:
                                                                                                                                                                                                        US-10-793-626-2774
                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOPTWARE: Patentin Ver. 2.1
SECTION 02774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2774, Application US/10793626 Publication No. US20050255478A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE: THEORY OF ARTIFICIAL Sequence: Synthetic OTHER INFORMATION: Description of Artificial Sequence OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 1847.1002
CURRENT APPLICATION NUMBER: US/11/051,720
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1780
SEQ ID NO 1375
LENGTH: 273
TYPE: PRT
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Publication No. US20060046257A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER
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TITLE OF INVENTION: MOVEL NUCLECTIDE AND AMINO ACID SEQUENCES,
TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 1847.1002
CURRENT APPLICATION NUMBER: US/11/051,720
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1780
SEQ ID NO 1373
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TYPE: PRT
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                              aAspGlyLysTrpHisArgValAlaIleSerValGluLysLysThrValThrMetIleVa 180
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US-11-051-720-1374
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         Sequence 154, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1780
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TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES,
TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 1847.1002
APPLICANT: KIMMERLY, WILLIAM JOHN
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TYPE: PRT
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Sequence 1372, Application US/11051720
publication No. US20060046257A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: NOVEL NUCLEOTIDE AND ITILE REFERENCE: 1847.1002
CURRENT APPLICATION NUMBER: US/11/051,720
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US-10-768-093-4 (1-527) x US-10-793-626-154 (1-1006)
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PRIOR FILING DATE: 1999-11-09
NUMBER OF SEO ID NOS: 4472
SOFTWARE: PATENTIN VET. 2.1
SEO ID NO 154
LENGTH: 1006
TYPE: PRT
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NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, THEREOF FOR DIAGNOSIS OF LUNG CANCER
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                               AND ASSAYS AND
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                                                                                                                                                                                                                                                                                                              501
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                                  METHOD
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CURRENT FILING DATE: 2005-01-27
INUMBER OF SEQ ID NOS: 1780
SEQ ID NO 1372
LENGTH: 1081
TYPE: PRT
ORGANISM: Homo Bapien8
US-11-051-720-1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-768-093-4 (1-527) x US-11-051-720-1372 (1-1081)
                                                                                                                                                                                                                                                                                                                                                                                                                                    "260 TCCTGAAAATGTATCCCAGGTAACGGTC-----TACCCTGTTTAT-----
                                                                                                                                                                                                                                                                                      140 uAspHisThrGlyLysProAlaProGluAspTyrProLeuPheArgThrValAsnIleAl 160
                                                                                                                                                                                                                                                                                                                                   120 nGluHisGlyIleGlnGinIleGlyValGluValGlyArgSerProValPheLeuPheGl 140
  200
                                                 180 lAspCysLysLysLysThrThrLysProLeuAspArgSerGluArgAlaIleValAspTh 200
                                                                                                                                             398 AGATCATGGTGCAGAGGTTACACCTAATCAACAATAACTTTTAAAGCGCTGAATTATAC 457
                                                                                                                                                                                       100 rIleLeuPheThrValLysProLysLysGlyIleGlnSerPheLeuLeuSerIleTyrAs 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 A------AAGGAAGGAGCTTTATTATTTAGTGTGAACTTAACTGT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 -AGTTTTTTGCACCTGAACCACGAATACAGCCT-----TCTTTTGGTGAAAATGTTGG. 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 TGCCAGAACAGAAATAGCGACTAAAAACTTCCCAGTATCAACGACTATTTCAAAA----- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 aGlnLeuSerAlaProThrLysGlnLeuPheProGlyGlyThrPheProGluAspPheSe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CyeThrAsnArgLysAsn-SerLysGlySerAspThrAlaTyrArgValSerLysGlnAl 80
                                                                                                                                                                                                                                       TGATGCTTCCCAATCAATAATCTACCAGATTGTTGATGAGAAAGGGGAAAAAAATGTTAAA 397
rAsnGiyIleThrValPheGlyThrArgileLeuAspGluGluValPheGluGiy 218
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73.50
40.9#
23.9#
7.8#
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                      299
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Search completed: April 10, 2006, 10:13:35 Job time: 23 Becs